

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 23, 2005, 09:41:05 ; Search time 260 Seconds
(without alignments)
5588.514 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 1202784 segs, 81838359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysts of the total score distribution.

SUMMARIES

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2	4547	100.0	3111	4	US-09-825-147-3
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8	1792.5	39.4	3287	3	US-09-105-058C-19
9	1790.5	39.4	2169	3	US-09-105-058C-22
10	1788	39.3	3232	3	US-09-177-650-1
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ALIGNMENTS

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RESULT 1
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Alignment Scores:
Pred. No.: 0
Score: 4547.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)
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RESULT 2
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; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. 6767736e1 Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

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Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

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QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1905 GACATCTATCAACAGAGCTCTTCGAAAGGCTCTGCTCAGCCCTCCCTTGGCTTCATTC 1964
QY 601 GlnIleProProPheGlnCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCCACTTTTAAATGTGAACAGACATCTGATTAACAAAGCCCTGTGATAGCAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTCCGGGTTCCGCACAAAACAGTGGCTGTTTCCAGATCAACATGAGCAAAATC 2084
QY 641 SerArgGlyLeuGlnIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGGCTCGAGTTCATTCGACGCCAAATGAAATTCAGTCCAGACTTTTCAACGG 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2145 CTTAAGCCCTACTGTGACAGTCAAGCAACAGAGTCCCAATTAAGTCAAAAGCAATGAGCTTA 2204
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2205 GGAGTGGCAGCCCAACACCAATTGCAAACTAAATATACGGCAACCAAGCCAGAGAGCC 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACTTTACAGATCCACACTCTCTCCAGCAGCATCAAGATCTGGCCAGGCGCAGAA 2324
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
Db 2325 ACTCTGCACCCCTAACCCCTGACAGGCTTAACGAAAGCAATTTCTGACGTCAACCACTGCTT 2384

QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTGCCTCCAAAGAAATGTTCAAGTTGCACAGTCAAAATCTCACCAAGACCGTTCTATAG 2444
QY 761 ArgLysSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysProMetValProLys 780
Db 2445 AGGAAACCTTTGACATGAGAGGAGAAACCTGTGTGTCTGTCTGTCCATGATGCTCCGAG 2504
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleAsnSerThrGlnGlnLeuAsnIle 800
Db 2505 GACTTGGGCAATCTTTGTCTGTGCAAACTGATCAGTGCAGCCGAGAACTGAATATA 2564
QY 801 GlnLeuSerGlySerGlnSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
Db 2565 CAACCTTCAGGAGAGTGAAGTCAAGTGTCTCCAGAGCAGCAAGATTTTACCCCAAAATCG 2624
QY 821 ArgGlnSerLysLeuPheIleThrAspGlnGlnValGlyProGlnGlnThrGlnThrAsp 840
Db 2625 AGGGAATCCAAATTTGTTATTAATGATGAAGAGGTGTCCCGAAGAGACAGACAGAC 2684
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTGATGCCGACCCGACGCTGCGCAGGAGAGCTGCTTTGCATCAGACTCTTAAG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGlnSerThrAspAlaLeu 880
Db 2745 ACTGGAAGTCAAGATCATCTCAGAGCAATTTGTAAAGCAGAGAAATGACAGATCCCTC 2804
QY 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-590-304-1 (1-3137)

QY 1 MetLysAspValGlnSerGlyArgGlyValLeuLeuAsnSerAlaAlaIleArgGly 20
Db 1 ATGAAGAGTGTGAGTCCGGCCCGGGCCAGGGTGTCTGAACTCGGACCGCCGAGGGGC 60
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlnGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGTACTGTGCTGGGACCGCGCGGCGCAAGCTCGGTGGGGGGGGGGGGCTG 120
QY 41 ArgGlnSerArgArgGlyLysGlnGlnValAlaArgMetSerLeuLeuGlyLysProLeuSer 60

121 AGGAGAGCCGCGGGGACAGAGGGGGCCCGATGAGCTGCTGGGGAAGCCGCTCTCT
QY TyThrSerserGlnSerCybaArgAAsnValIlystrArgArgValGlnAsnTrpLeu 80
Db TACACGAGTGGACGAGACCTCGCGGACAGCTCAAGTACCGGGGGGCAACTACCTG 240
QY TyAsnValIleuGluAProArgGlyTrpAlaPheIleThrIleAlaPheValIleLeu 100
Db TACACGAGTGGAGAGACCCCGGGGCGGTGATCATCAACGCTTTCGTTTTCTC 300
QY LeuValPheGlyCybLeuIleLeuSerValPheSerThrIleProGlnIleThrIlyLeu 120
Db CTGTGCTTGGTGGCTGATTTTGTACGTGTTTTCTACCATCCCTGAGCACAAATTTG 360
QY AlaSerSerCybLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db GCCTCAAGTTCCTCTTGATCTCGAGTTCGTATGATTCGTCTTGGTTGGAGTTTC 420
QY IleIleArgIleThrSerAlaGlyCybCybArgTrpArgIleTrpGlnIlyArgLeu 160
Db ATCATTCGAATCTGGTTCGGGGTGTCTGTTCGATATAGAGATGGCAAGAGACTG 480
QY ArgPheAlaArgIlySPropheCybValIleAspThrIleValIleuIleAlaSerIleAla 180
Db AGGTTTGCTGGAAGCCCTTCTGTGTTATAGATACCATTCCTTATCCCTCAATAGCA 540
QY ValValSerAlaIlyThrGlnIlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db GTTGTTCTGCAAAACTCAGGGTAATATTTTGGCCAGTCTGACACAGAACTCCCT 600
QY PheLeuGlnIleLeuArgMetValArgMetAspArgArgIlyGlyIlyThrIlyPheLeu 220
Db TTCTTACAGATCTCGCATGTGGTGGCATGACCGAAGGGGAGGCACTTGGAAATTA 660
QY GlySerValValIlyAlaIleSerIlyGluLeuIleThrAlaTrpIlyIleGlyPheLeu 240
Db GGTTCAGTGGTTATGTCTACACAGAGATTAATCAAGCTTGATACATAGATTTTGG 720
QY ValLeuIlePheSerSerPheLeuValIlyLeuValGluIlyAsnAlaAsnIlyGluPhe 260
Db GTTCTTATTTTTCGCTTTCCTTGTCTATCTGTGGAAAGAGATGCATTAAGAGTTT 780
QY SerThrTrpAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrIleGlyTrpGly 280
Db TCTACATATGCAATGCTCTCTGTGGGGGACAAATTAATCAATATGCTATGGA 840
QY AspIlyThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db GACAAACCTCCCTAAGCTTGGCTGGGAGATTCCTTTCTGCAAGCTTTCGACTCTTGGC 900
QY IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuIlyValGln 320
Db ATTTCTTCTTCTGACCTTCTGCGGCAATCTTGGCTCAGTTCGATTTAAAGTACAA 960
QY GluGlnIleArgGlnIlyHisPheGluIlyArgArgAsnProAlaIleAsnLeuIleGln 340
Db GAACACACCGGCAAGAACCTTTGAGAAAGAGAGAACCCAGCTGCAACCTCATTTG 1020
QY CybValIlyPheSerTrpAlaAlaAspGluIlySerValSerIleAlaThrTrpIlyPro 360
Db TGTGTTTGGGTAGTTACCGCAGCTGATGAGAAATCTGTTTCCATTCGACCTGGAAGCCA 1080
QY HisLeuLeuValAlaLeuHisThrCybSerProThr----- 371
Db 1081 CACTTAAAGGCTTTCACACCTCAGCCCTTACCAAGAAAGAACAGGGAAGCATCAAG 1140
QY AsnGlnIlyLeuSerPheIlySGluArgValArgMetAlaSerProArgIlyGlnSerIle 391
Db 1141 AGTCAGAAAGTAACTTTTAAAGAGCAGAGTCCGATGCTAGCCCGGAGGAGGAGTATT 1200
QY LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGAGGTCCCAAGCACGACATCACAGCCGAG 1260
QY GlySerProThrIlyValGlnIlySerTrpSerPheAsnAspArgThrArgPheAlaPro 431
Db 1261 GGCAGTCCACCAAAATGACAGAGAGAGTGAAGCTTCAAGACGGAACCCGCTTCGGCCC 1320
QY SerLeuArgLeuIlySerSerGlnProIlyProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTCGCCTCAAAAGTTCTCAGCCCAACAGTATGATGCTCAACAGCCCTTGGC 1380
QY ThrAspAspValIlyArgPheGluIlySGlyCybGlnCybAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATGATATATGATGAAAGAGTCCAGTGTGATGATGATGAGAGACCTCACCC 1440
QY ProProLeuIlyThrValIleArgAlaIleArgIleMetIlyPheHisValAlaIlyArg 491
Db 1441 CCACCACTTAAACCTGCTATCGAGTATCAAGAAATTAATTAATTCATCTTCCAAACCG 1500
QY LysPheIlyGluThrLeuArgProIlyArgPheValIleGluGlnIlyTrpSerAla 511
Db 1501 AAGTTTAAAGAAACATTAAGTCTCATATGATGATGATGATGATGATGATGATGATGAT 1560
QY GlyHisLeuAspMetLeuCybArgIleIlySerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCACTGAGACATGTTGTGTAATTAAGGCTTCAAAACGATGTGATCAAAATTTCTT 1620
QY GlyIlySGlyGlnIleThrSerAspIlySerArgGluIlyIleThrAlaGluIlySGlu 551
Db 1621 GGAAAGGGCAAAATCATCAATTAAGAGACCGGAGAAATTAACACAGCAAGCTAGAG 1680
QY ThrThrAspAspLeuSerMetLeuGlyArgValIleIlyValGluIlySGlnValGlnSer 571
Db 1681 ACCACAGACATCTCATATGCTCGGTGGGTGTCAGGTTGAAAACAGGTACAGTCC 1740
QY IleGluSerIlyLeuAspCybLeuLeuAspIleIlyGlnGlnValLeuArgIlySGlySer 591
Db 1741 ATAGAAATCCAGCTGAGCTGCTTACATCTATCAACAGGTCTCTTGGAAAGGCTCT 1800
QY AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluIlyGluGlnThrSer 611
Db 1801 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTGAAGTGAACAGACATCT 1860
QY AspIlyGlnSerProValAspSerIlyAspLeuSerGlySerAlaGlnAsnSerGlyCyb 631
Db 1861 GACTATCAAGCCCTGTGATAGCAAAAGTCTTTGGGGTTCGGCACAAACGTGCTGC 1920
QY LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATCCAGATCAACTAGTCCAAATCTCGAGAGGCTTCAGATTCCTGACGCCAAAT 1980
QY GluPheSerAlaGlnThrPheTrpAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 GAGTTCAGGCCCAAGCTTTCATACGGCTTACCCCTTACATATCAACAGTCAACACACAG 2040
QY ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2041 GTGCCAATTAATGCAAGCATGGCTCAGCAGTGGGACCAACCAACCTTGGCAACCA 2100
QY IleAsnThrAlaProIlySerProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2101 ATTAATACGGCACCCCAAGCAGCAGCCCAACCAACTTTCAGATCCCACTCTCCCA 2160
QY AlaIleIlyHisIleuProArgProGluThrIleuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2161 GCATTCACAGCATCTGCCGAGCAAAATCTTGCAACCTTCAGAGCTTAAACAGAA 2220
QY SerIleSerAspValIlyThrCybLeuValAlaSerIlySGluAsnValGlnValAlaGln 751
Db 2221 AGCATTTTCAAGTCAACCACTGCTTGTGCTCCAGAGAAATGTTTCAGGTTGCACAG 2280
QY SerAsnLeuThrLysAspArgSerMetArgIlySerPheAspMetGlyGlyIlyThrLeu 771
Db 2281 TCAAAATCTACCAAGACCGTTCATGAGAAAACTTTGATGATGAGAGAAACTCTG 2340

QY 772 LeuSerValCySPrometValProLyAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
| | | | |
Db 2341 TTGTCGTCTGTCCTCCATGGTGGCGAAGGACTTGGGCAAAATCTTTGCTCTGGCAAAACCTGG 2400
| | | | |
QY 792 TLeaYSerThrGlnGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
| | | | |
Db 2401 ATCAGGTCACCGAGGAACTGTAATATACACTTTCGAGGAGTGAAGCAAGTGGCTCCAA 2460
| | | | |
QY 812 GlySerGlnAspPheTyProLySerProLySerGlyLeuPheIleThrAspGlnGlu 831
| | | | |
Db 2461 GGCAGCGCAAGATTTTATCCCAATGAGGGAAATCCAAATGTTTATTAATCATGATGAAG 2520
| | | | |
QY 832 ValGlyProGlnGluThrGlnThrAspThrPheAspAlaIleProGlnProIleArgGlu 851
| | | | |
Db 2521 GTGGGTCGCCAGAGACAGACAGACACTTTGATGCCGACCGCAGCCGCGCAGGGAA 2580
| | | | |
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
| | | | |
Db 2581 GCGCTTTGCAATCAGACTCTCTTAAGGACTGGAAGGTCAATCATCTCAGAGCAATTTGT 2640
| | | | |
QY 872 LysAlaGlyLysSerThrAspAlaLeuSerLeuProHleValLysLeuLys 888
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Db 2641 AAGCGAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAAA 2691
| | | | |
RESULT 4
US-09-813-148-1
/ Sequence 1, Application US/09813148
/ Patent No. 6617131
/ GENERAL INFORMATION:
/ APPLICANT: STEINMEYER, Klaus
/ APPLICANT: LERCHE, Christian
/ APPLICANT: SCHERER, Constanze
/ APPLICANT: SEEBOW, Guiscard
/ APPLICANT: BUSCH, Andreas E.
/ TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CEN
/ TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
/ FILE REFERENCE: 38005-119
/ CURRENT APPLICATION NUMBER: US/09/813,148
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: DE 100 13 732.6
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/194,041
/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-148-1
Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
Gaps: 1
US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

QY 61 TyrThrSerSerGlnSerCysArgHrsAnValLysTyrArgArgValGlnAsnTyrLeu 80
| | | | |
Db 395 TACAGAGATGACGAGAGCTGGCGGCGCAACGTCAAGTACCGCGGGCTGCAGAACTACCTGG 454
| | | | |
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
| | | | |
Db 455 TACAACGGCTGGAGAGACCCCGCGGCGGCTTCATCTACACGCTTTCGTTTCTCTC 514
| | | | |
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHleThrLysLeu 120
| | | | |
Db 515 CTGTCCTTGGGCTTGAATTTTTCAGTGTTCCTACCAATCCCTGAGCACCAAAATTTG 574
| | | | |
QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValIlePheGlyLeuGlnPhe 140
| | | | |
Db 575 GCCTCAAGTTGCTCTTGCATCTGAGATTCGAGATTTGTCGTCTTGTGGAGTTTC 634
| | | | |
QY 141 TlelleaGllleTPrSerAlaGlyCysGlySerArgTyrArgGlyTyrGlnGlyArgLeu 160
| | | | |
Db 635 ATCAATTCGAATCTGGTCTGGCGGTTGCTGTTGTCATATAGAGATGGCAAGAAAGACTG 694
| | | | |
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
| | | | |
Db 695 AGCTTGTCTCAAAACCTTCTGTGTTATAGATACATGTTTCTTATCGCTTCAATACGA 754
| | | | |
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrLysLeuLeu 220
| | | | |
Db 755 GTTGTTCGCAAAAACCTCAGGGTAAATTTTGGCAGCTCGCAGCTCAGAAATCTCCGT 814
| | | | |
QY 815 TTCTTACAGATCTCCGATGATGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
| | | | |
Db 221 GlySerValValTyrAlaHleSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeu 240
| | | | |
QY 875 GGTTAGAGGTTTATGCTCACAGAGAAATTAATCACAGCTTGGTATAGATTTTGG 934
| | | | |
Db 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAlaAsnLysGlnPhe 260
| | | | |
QY 935 GTTCTTAATTTTTCGCTTCTTCTGTCATCTGGTGGAAAGATGCAATTAAGAGTTT 994
| | | | |
Db 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
| | | | |
QY 995 TCTACATATGAGAGATGCTCTGAGGGGCACAATTAATTAATGACACTATATGGCTATAGA 1054
| | | | |
Db 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
| | | | |
QY 1055 GACAAAACCTCCCTTAATCTTGGCTGGAAAGATTTGTTCTGCAGGCTTTCCTCTGGC 1114
| | | | |
Db 301 TLeSerPhePheAlaLeuProAlaGlyTyrLeuGlySerGlyPheAlaLeuLysValGln 320
| | | | |
QY 1115 ATTTCTTCTTGGACCTTCGCGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAA 1174
| | | | |
Db 321 GlnGlnHleAsArgGlnLysHlePheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
| | | | |
QY 1175 GAAACAACCCCGCAGAAACACTTTGAGAAAGAAAGAAACCAAGCTGCCAACCTCATTAAG 1234
| | | | |
Db 341 CysValTyrPArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTrpLysPro 360
| | | | |
QY 1235 TGTGTTTGGCGTAAGTTACGCACTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1294
| | | | |
Db 361 HleLeuLysValAlaLeuHleThrCysSerProThr----- 371
| | | | |
QY 1295 CACTTGAAGGCTTGGCAACCTGAGCCCTTACCAAGAAAGAAAGAGGGAAGCATCAAGC 1354
| | | | |
Db 372 AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyGlnSerIle 391
| | | | |
QY 1335 AGTCAGAAAGCTTAAGTTTAAAGAGCGAGTGGCAATGCTTAACCCAGGAGGCAAGATTT 1414
| | | | |
Db 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
| | | | |
QY 1415 AAGAGCGAGCAAGCTCAGTATGATGAGACAGAGGTCCCAACACCGAATCATCAGCCGAG 1474
| | | | |

QY 412 GlySerProThrIysValGlnIysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
 Db 1475 GGCAGTCCCAAGAGGAGAGAGCTGGAGCTTCAACGACCGACCTCCGGCCC 1534
 QY 432 SerLeuArgLeuIysSerSerGlnProIysProValIleAspAlaAspThrAlaLeuGly 451
 Db 1535 TCCCTGGCCCTCAAAAGTTCTCAGCCCAAAACAGTGTATGATCTGCACAGCCCTTGGC 1594
 QY 452 ThrAspAspValIyrAspGluIysGluIysGluIysAspValSerValGluAspLeuThr 471
 Db 1595 ACTGATGATGATATGATGATAAAGATGCGCAGTGTATGATATCAGTGAAGACCTCACC 1654
 QY 472 ProProLeuIysThrValIleArgAlaIleArgIleMetIysPheHisValAlaIysArg 491
 Db 1655 CCACCACTTAAACCTGTCATTCCAGCTATCAGAAATTATGAATTTCATGTTGCAAAACGG 1714
 QY 492 LysPheIysGluThrLeuArgProIyrAspValIysAspValIleGluGlnIyrSerAla 511
 Db 1715 AAGCTTAAAGGAACATTACCTCCATGATGTAAAGATCTCATTCGMAACAATATTCGCT 1774
 QY 512 GlnHisLeuAspMetLeuIysArgGluIysSerLeuGlnThrArgValAspGlnIleLeu 531
 Db 1775 GGTCACTTGACAGTGTGTGTAAGATTAAAGCCTTCAACAGGTGTGATCAAAATTCCT 1834
 QY 532 GlyIysGlyGlnIleThrSerAspIysIysSerArgGluIysIleThrAlaGluHisGlu 551
 Db 1835 GGAAGAGGCAAAATCATTCACTAGTATGAAGAACGCCGAGAAATTAACAGCAGAACATGAG 1894
 QY 552 ThrThrAspAspLeuSerMetLeuGluIysArgValIysValGluIysGlnValGlnSer 571
 Db 1895 ACCACAGACCATCTCAGTATGCTCGGTCGGGTGTCAGAGTTGAAAAACAGTACAGTCC 1954
 QY 572 IleGluSerIyrLeuAspCysLeuLeuAspIleIyrGlnGlnValLeuArgIysGlySer 591
 Db 1955 ATAGAAATCCAGGTGAGCTGCTCACTAGCATCTATCAACAGATCCTTCGGAAGGCTCT 2014
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
 Db 2015 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCACCTTTGAATGTGAACGACATCT 2074
 QY 612 AspTyrGlnSerProValAspSerIysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 2075 GACTATCAAAAGCCCTGTGATACAAAGATCTTCCGGGTTCCCAACAAACATGTGCTGC 2134
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgIylLeuGlnPheIleuThrProAsn 651
 Db 2135 TTATCCAGATCAACTAGTGCACATCTCGAGAGCCTGCAGTTCAATTCGACGCCAAAT 2194
 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 2195 GAGTTCACTGCCAGACTTTCTACGCCCTTAGCCCTTAGTGCACAGTCAAGCAACACAG 2254
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
 Db 2255 GTGCCAATTAGTCAAAAGCGATGCTCAGCAGTGGCAGCCCAACACCAATTCGCAACCAA 2314
 QY 692 IleAsnThrAlaProIysProAlaAlaProThrThrLeuGlnIleProProPheLeuPro 711
 Db 2315 ATAAATACGGCAGCCAGCAGCAGCCCAACCACTTACAGATCCCACTCTCTCCCA 2374
 QY 712 AlaIleIysHisLeuProArgProGluThrLeuHisProAsnProAlaGluLeuGlnGlu 731
 Db 2375 GCATCAAGATCTGCCAGGCGCAAGAACTCTGCACCCCTACAGCTCAGGCTTACAGGAA 2434
 QY 732 SerIleSerAspValIThrThrCysLeuValAlaSerIysGluAsnValGlnValAlaGln 751
 Db 2435 AGCATTTCTGACCTCAACACCTGCTGTGCTCCCAAGGAAATGTTCCAGGTGACACG 2494
 QY 752 SerAsnLeuThrIysAspAspSerMetArgIysSerPheAspMetGlyGlyGluThrLeu 771
 Db 2495 TCAAACTTCAACCAAGGACCGTCTCTATGAGGAAAAAGCTTGAACATGGAGGAGAACTCTG 2554
 QY 772 LeuSerValCysProMetValProIysAspLeuGlyIysSerLeuSerValGlnAsnLeu 791

Db 2555 TTGTCTGTCTGTCCTCCATGGTGGCCGAAAGCACTTGGGAAATCTTTGCTGTGCAAAACCTG 2614
 QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
 Db 2615 ATCAGGTTCACCGAGAGAACGTGAATATATCAACTTTCAGGAGATGAGTCAAGTGGCTCCAGA 2674
 QY 812 GlySerGlnAspPheTyrProIysTrpArgIysSerIysLeuPheIleThrAspGluGlu 831
 Db 2675 GGCAGCCAGATTTTATCCCAATGAGAGGAAATCCAAATTTGTTATATCTGATGAAGAG 2734
 QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
 Db 2735 GTGGGTCCCGAAGACACAGACAGACACTTTTGTAGTGGCGCACCCGACCTGCCAGGAA 2794
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyIysArgSerArgSerSerGlnSerIleCys 871
 Db 2795 GCTGCCCTTTCATCAACACTCTCTAAGGACTGGAAGTCAAGATCAATCTCAGAGCATTTGT 2854
 QY 872 LysAlaGluGluSerThrAspAlaLeuSerLeuProHisValIysLeuIys 888
 Db 2855 AAGCGAGGAAGATRCAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA 2905
 Db 2855 AAGCGAGGAAGATRCAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA 2905
 RESULT 5
 US-09-492-361-1
 ; Sequence 1, Application US/09492361
 ; Patent No. 6794161
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTSCH, Thomas J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
 ; FILE REFERENCE: 2815-127P
 ; CURRENT APPLICATION NUMBER: US/09/492,361
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2335
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: gene
 ; LOCATION: (1)..(2335)
 ; NAME/KEY: CDS
 ; LOCATION: (83)..(2170)
 US-09-492-361-1
 Alignment Scores:
 Pred. No.: 5,98e-203 Length: 2335
 Score: 2007.50 Matches: 434
 Percent Similarity: 65.32% Conservative: 82
 Best Local Similarity: 54.94% Mismatches: 133
 Query Match: 44.15% Indels: 141
 DB: 4 Gaps: 16
 US-09-810-796-5 (1-888) x US-09-492-361-1 (1-2335)
 QY 8 ArgIysArgValLeuLeuAsnSerAlaAlaArgGlyAspGlyLeuLeuLeuLeuGly 27
 Db 127 CGGGAGCGCCCGCGCGAGCTAGTGGCTCAGGC----- 165
 QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGluSerArgArgGlyIys 47
 Db 166 ---CGTCAGACGAAACAGAGCGGAGCGGG-----CGGGGCGG 201
 QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyIysProLeu----- 59
 Db 202 CTCGCCGCGCGCTCGGCTCTCTGGGCGAGCCCTCGCGCGCGGCGCCCTCCCTGG 261
 QY 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValIysTyr 73
 Db 262 GCCGGGCTCCGGCTCGGGCTCGGCTCGGCGGCGGAGGCTTCCTGGCGCGGACAGACGCTTA 321

[illegible]

Db	1402	CCGATGGGACGCTCCAGCGCGGAGCGGCTCTCCAAAGCAGAGCTGCACCTCCAC	1461
Qy	339	YASPARgRgSerProSerThraP11ethrAlaGluGly--SerProThrlYsValG1	418
Db	1462	AATGCCCACTCCCCAAGCAGCGAGCGAGTGGTGAAGCCACCAAGCCCCACCAAGGTGCA	1521
Qy	418	nlySerTrpSerPheAsnAPaRgTTrARgPheARgProSerLeuThrlYsSerSe	438
Db	1522	AAAGAGCTGGAGCTTCATAGCCGACCCGCTTCGGGACATCTTGAGACTC-----	1573
Qy	438	rGlnProLySProVal11leaPalaSerThrAlaLeuGlyThraSPaPValYraSPg1	458
Db	1574	-----AAACCCCGCACTCTGCTGAGATGCC---CCCTCAAGAGAAGTACAGAGGA	1623
Qy	458	uLyGlyCyseGlnYsAspValSerValGluAspLeuThrProProLeuThrlY11	478
Db	1624	GAAGAGCTACAGTGTAGCTCAGCGTGAAGCAGCATATGCTGTGTGAAGACATCAT	1683
Qy	478	eARgAla1leArg11leMeLySPheH1sValAlaYsARgYpHeLySGluThrLeuAR	498
Db	1684	CGCGTCATTCAGATTCCTCAAGTTCCTGTTGGCCAAAAGAAATTCAAAGAGACACTGCG	1743
Qy	498	gProTyraSPValYsAspVal11leGluGlnTyRserAlaGlyH1sLeuSPheLeuCy	518
Db	1744	ACCGTACACACTGAAGAGCGTCATTTGACAGTATCTCAGCGGCCACTTGACATGCTGGG	1803
Qy	518	sARg11eLySerLeuGlnThraRgValaSPGln1leuGlyLySGlyGln1leThrSe	538
Db	1804	CCGATACAGAGCTTCGAACTCGGCTGGACCAAAATTCGTGGTCCGGGG-----CCCG	1857
Qy	538	rAsp1yLySeRarg1u-----Lyel1eThrAlaGluH1sGluThrThraSPas	555
Db	1858	GGACAGGAGGCGCCGGAGAAAGGCGCAAGAGGCGCCCTCCGACCGGAGGTGTGATGA	1917
Qy	555	pLeuSerMetLeuGlyThraValYalYsValGluLySGlnValGlnSer11leGlySerLy	575
Db	1918	AATCAGCATGTATGGAGCGCTGTGCATAGTGAAGAAACAGAGTGCATCTCAGACACAA	1977
Qy	575	sLeuAspCySleuLeuAsp11eTyrgGlnGlnVal1leuARgLySG1ySerAlaSerAlaLe	595
Db	1978	GCTGGACTGTGTGGCTTCATATCGCGCTGCTCGCTGTGGACCTCGGCC-----	2032
Qy	595	uAlaLeuAlaSerPheGln1leProProPheGluCySGluGlnThrSerAPryGlnSe	615
Db	2033	-AGCTGGGCGCCCTGCAGAGTCCGCTGTTGCAGCCGACATCACTTCGACTACACAG	2091
Qy	615	rProValaSPserLySAspLeuSerG1ySerAlaGlnAsnSerG1yCySLeuSerARgSe	635
Db	2092	CCCTGTGGACACAGAGGACATCTCCGTCTCGGCACAAACCTGAC--ATCTCCGCTC	2148
Qy	635	rThSerAlaAsn1leSerARg1yLeuGlnPhe1leuThrProAsnGluPheSerAl	655
Db	2149	GGTCAGACCAACAACTGACTGAGGG-----	2173
Qy	655	aGlnThrPheYrAlaLeuSerProThrMetH1sSerGlnAlaThrGlnValPro11eSe	675
Db	2174	-----ACTTC	2178
Qy	675	rGlnSerAspG1ySerAlaValaAlaAlaThraSnrThrl1eAlaAsnGln1leAsnThra1	695
Db	2179	TCAGAGGAGGAGGACAGACA-----CGGCACAG	2205
Qy	695	aProLySProAlaAlaProThrThrlLeu-Gln1leProProProLeuProAla1leYsh	715
Db	2206	CCCCGGGCTGGCGCTCTCGACTGCCCTCTTAAGGCTCCGAGCTCTCTCGACTTGAAC	2265
Qy	715	1sLeuProARgProGluThrLeuH1s	723
Db	2266	CACCTCCCTCAACGGGAGAGAGACAC	2291

Sequence 1823, Application US/09949016
 Patent No. 6812319
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1823
 LENGTH: 2196
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-1823

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Db      1687 CGGGTGGACCAATTGGGTGGGG-----CCCGGGAGACGAGAGCCCGGGAGAG 1740
QY      545 -----LysIleThrAlaGlnHisGluThrThrAspAspLeuSerMetLeuGlyArgVal 562
Db      1741 GCGGACAGAGGGGCGCTCCGACGGGAGGCTGGTGAATGAAATCGATGATGGACCGCTG 1800
QY      563 ValIysValGluIysGlnValGlnSerIleGluSerIysLeuAspCysLeuLeuAspIle 582
Db      1801 GTCAAGGTGAGAAAGCAGGTGACATCCATCGACACAGCTGACCTGGCTGTGGGCTTC 1860
QY      583 TyrGlnGlnValLeuArgIysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIle 602
Db      1861 TATTCCGCTGCTGGCTCTGGCACCTCGGC-----AGCCTGGGCGCCGCTGCAGAG 1914
QY      603 ProProPheGluCysGlnThrSerAspTyrGlnSerProValAspSerIysAspLeu 622
Db      1915 CCGCTTTGACACCCGACATCACTCCGACTACCAAGCCCTGTGACCAAGAGACATC 1974
QY      623 SerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArg 642
Db      1975 TCCGCTCCGACAGACGCTCAGC---ATCTCCGCTCGGTGAGCACCAACATGCACTGA 2031
QY      643 GlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSer 662
Db      2032 GGG----- 2034
QY      663 ProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaVal 682
Db      2035 -----ACTTCTCAGAGGAGGAGGACAGCA---- 2058
QY      683 AlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProIysProAlaAlaProThr 702
Db      2059 -----CGGCGACCGCCCGCGCTGCGCTCCGACT 2088
QY      703 ThrIeu-GlnIleProProProLeuProAlaIleIysHisLeuProArgProGluThrIe 722
Db      2089 GCCCTTGAGGCTCCGAGCTCTCTGTAATTGAATCACTCCCTCACGGGAGAGAGA 2148
QY      722 uHis 723
Db      2149 CCAC 2152

RESULT 7
US-09-177-650-95
; Sequence 95, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2917)
US-09-177-650-95

Alignment Scores:
Pred. No.: 6,32e-180 Length: 3337
Score: 1794.00 Matches: 432

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Percent Similarity: 56.22% Conservative: 106
Best Local Similarity: 45.14% Mismatches: 225
Query Match: 39.45% Indels: 195
DB: 3 Gaps: 26

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QY      37 GlyIysGlyLeuArgGlnSerArgArgGlyIysGlnGlyAlaArgMetSerLeuLeuGly 56
Db      278 GGCACACATCTTCAACAACCTCGCGCGGCGCGCGCGCGCC-----GGG 322
QY      57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgVal 76
Db      323 AAGCC-----CCCAAGCCCAAGCCCTTCTACCGCAAGCTG 358
QY      77 GlnAsnTyrLeuTyrAsnValLeuGlnIuArgProArgIYThrAlaPheIleTyrHisAla 96
Db      359 CAGAAATTCCTTACCAAGCTGCTGAGCGCGCGCGCTGGGCTTCATCAACACGCC 418
QY      97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db      419 TACGTGTTCTCTGGTTTCTCTGCTCGCTGCTGTGTGTTTCCACCATCAAGAG 478
QY      117 HisThrIysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValIlePhe 136
Db      479 TATGAGAAAGAGCTCGGAGGGGCGCTTACATCTCGGAATCGTACATGCTGTGTTT 538
QY      137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db      539 GCGGTGAGAGTACTTGTGCTGGATCGGACCGCGCGCTGCTGCGGTACCGGTGCTGG 598
QY      157 GlnGlyArgLeuArgPheAlaArgIysProPheCysValIleAspThrIleValLeuIle 176
Db      599 AGGGGGCGGCTCAAGTTGGCCCGGAAACGGTGTGTGATGATGATCATGATGCTGCTATC 658
QY      177 AlaSerIleAlaValAlaSerAlaIysThrGlnGlnIlePheAlaThrSerAlaLeu 196
Db      659 GCCTCATTTGGGGTCTGCGCGCGCGCGCTCCAGGCAACGTTTGGCACATCTGCGCTC 718
QY      197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgIyGlyThr 216
Db      719 CGGAGCTCGCGCTCTCGACATTCGCGAGTGAATCCGACATGAGACCGCGGGAGGACAC 778
QY      217 TrpIysLeuLeuGlySerValValTyrAlaHisSerIysGluLeuIleThrAlaTrpTyr 236
Db      779 TGGAAAGCTGTGGGCTGTGTGTCTATGCCACAGACAGAGAGCTGTCACTGCTGTAC 838
QY      237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluIysAspAla 256
Db      839 ATCGCTTCTCTTGTCTCATCTGCGCTCGTTCGTGCTGCTGCTGCGAGAGAGGGGAG 898
QY      257 AsnIysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
Db      899 AAGCAACCACTTGAACCTTACCGCGGATCCACTGTGTGGGCGCTGTATACCGTGCACC 958
QY      277 IleGlyTyrGlyAspIysThrProLeuThrTrpLeuGlyArgGlyLeuSerAlaGlyPhe 296
Db      959 ATTGGCTACGGGAGCAATACCCCGACACTGTGAACGCGAGGCTCTTGGCGAACCTTC 1018
QY      297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db      1019 ACCCTCATCGGTGTCTCTTCTGCGCTGCTGAGCATCTTGGGTGCTGCTTGGCC 1078
QY      317 LeuIysValGlnGluGlnHisArgGlnIysHisPheGluIysArgArgAsnProAlaAla 336
Db      1079 CTGAAGGTTCAGAGCAGACAGGAGCACTTTGAGAAAGCGGAAACCCGCGACAGA 1138
QY      337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349

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Db 1139 GGCCTGATCCAGTCGGCTGAGATTTCTACGCCAACCTCTGCGCAGACCTGCAC 1198
Qy 350 -----GluYserValSerIleAlaThrIlePhe 359
Db 1199 TCACAGTCGACGATCTACGAGCGGACCGTACGTCATGTACAGTTCCGAAACTCAA 1258
Qy 360 -----ProIleLeuValLeuHISThr 367
Db 1259 ACCTAGGGGGCTCCAGACTTATCCCGCTGAACAGCTGAGCTGCAGAAACTTC 1318
Qy 367 ----- 367
Db 1319 AAGAGTAATCTGACTGCTTTACAGAGAACCCCGCGGAGCCCTCTCCAACTAA 1378
Qy 368 -----CysSerPro-----ThrAngIleuLeu 375
Db 1379 GGCAGCCCGTCGACAGGGCCCTGTGTGATGCTGCCCGGACGCTTACCCAGAAAGTC 1438
Qy 376 SerPheIleuValArgMetAlaSerProArgGlyIleSerIleYserArgGln 395
Db 1439 AGTTGAAAGATGCTGTCTTCTCAGCCCGGAGCGGTGCTGCAGAGGGAAGGG 1495
Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlyIleSer 413
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Qy 414 ProThrIleValGlnIleYserThrSerPheAsnAspArgThrArgPheArgProSerIleu 433
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Qy 434 ArgLeuIleYserSerGlnProIleValIleAspAlaAspThrAlaLeuGlyThrAsp 453
Db 1616 CGCATCAAGGTGCCCGGTACCGGAGAACTCAGAA---GAGCAAGACCTCCCGGAGAG 1672
Qy 454 AsnValIleYserGlyIleValGlnIleYserValIleValIleValIleValIleValIle 473
Db 1673 GACATTTGATGATACAAAGACTGCTCCCTGCGAGTTTGTGACCGAGGACCTGAGCCCGGCG 1732
Qy 474 LeuIleValThrValIleArgAlaIleArgIleMetIlePheHISValAlaValAspValPhe 493
Db 1733 CTCAAGATCAGATCAGAGCGGTGTGTGTATGCGGTCTGTGATGTCAGAGCGGAAGTTC 1792
Qy 494 LysGluIleThrLeuArgProIleYserValIleValIleGluIleIleYserAlaGlyHIS 513
Db 1793 AAGGAGAGCTGCGGCGCTTACGACGTGATGAGCTATCGAGAGTACTAGCGGCGCAC 1852
Qy 514 LeuAspMetLeuCyValArgIleYserLeuGlnThrArgValArgGlnIleLeuGlyIle 533
Db 1853 CTGACATGCTGCTTCCGGAATTAAAGAGCTGACGTCCAGAGTGCAGAGATCGTGGGCGG 1912
Qy 534 GlyGlnIleThrSerAspIleYserValIleValIleValIleValIleValIleValIle 553
Db 1913 GGCACGAGCTACGAGC---AAGAGCCGACCAAGGCGCGGCGGAGGAGCTGCC 1969
Qy 554 AspAspLeuSerMetLeuGlyArgValIleValIleValIleValIleValIleValIleValIle 573
Db 1970 GAGGAGCCCGACGATGAGGACCGCTCGGAGAGTGGAGAGAGAGTCTTGTCTCATAGAG 2029
Qy 574 SerIleLeuAspCyLeuLeuAspIleIleYserGlnValIleuArgIleYserAlaSer 593
Db 2030 AAGAACTGACTTCTCGTGAATATCTACATCAG---CGGATGGGC----- 2074
Qy 594 AlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys----- 607
Db 2075 -----ATCCCCCGACAGAGCCGAGGCTTACTTTGGGGCC 2110
Qy 608 -----GluGlnThrSerAspIleYserGlnIleValIleValIleValIleValIleValIle 624
Db 2111 AAGAGCCCGGAGCGGCGCGCTGACAGCCCGGAAGACAGCGGAGG----- 2161
Qy 625 SerAlaGlnAsnSerGlyCyLeuSerArgSerThrSerAlaAsnIleSerArgIleu 644
Db 2162 CATGTGACAGGACGCGTGCATTTGTCAAGATGCTGCGCTCCAGAGCTCCAGCGGC--- 2218

Qy 645 GlnPheIleuThrProAsnGluPheSerAlaGlnThrPheThrAlaLeuSerProThr 664
Db 2218 ----- 2218
Qy 665 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAla 684
Db 2218 ----- 2218
Qy 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProIleProAlaIleProThrIleu 704
Db 2219 -----CAGAAACTTCTCGCGCCCGCCCGCGCGCC---CCTGTC 2257
Qy 705 GlnIleProPro-----ProLeuProAlaIleYserHIS 715
Db 2258 CAGTGTCCGCTCCACCTCTGAGCCAGAGAGCCAGCCCGG---CCAGGCGCAGCGCAC 2316
Qy 716 LeuProArg-----ProGluThr-----LeuHIS-ProAsnProAlaGlyLeuGlnI 731
Db 2317 CTCCCGCGTGGGGGACACAGGCTCCTGGTGGCATCCGCGCGCTGCCAGCAGAGG 2376
Qy 731 uSerIleSerAspValIleThrCyLeuValAlaSerIleYserGluAsnValGlnValAla 751
Db 2377 GTGCTGTCCGCTACAGCGGGGCAACCGCGCAGCATGAGTTCTCGCGCAGAGGA 2436
Qy 751 nSerAsnLeuThrIleYser-----AspArgSerMetArgIleYserPheAspMetGlyIle 769
Db 2437 CACCCCGGCTGACAGGCCCGCCGAGGGAACCTCGGAGACAGC-----GA 2481
Qy 769 uThrIleuSerValCysProMetValProIleAspLeuGlyIleYserIleSerValG 789
Db 2482 CACGTCATCTCATCCGCTCGGTGAGCAGAGAGTGGAGCTTCTTCCAGCGGCTT 2541
Qy 789 nAsnLeuIleArgSerThrGluIleuAsnIleGlnLeuSerGlySerGluSerG 809
Db 2542 CAGCATCTCCAGTCCAGAGAAACCTGATGCTCAACAGCTGTACGCGCGCTGCG 2601
Qy 809 YserArgIleYserGlnAspPheIleYserProIleYserIleValIlePheIleThrAs 829
Db 2602 GCCTTGTGCCAAAGTACAGCCCTTACATTGCGAGGAGAGTACAGC-----ACCA 2652
Qy 829 pGluGluVal-----GlyPro-----GluGluThrG 838
Db 2653 CTCCGACCTCTGTACCCGCTGCGGCGCCCGGACGAGCTGCGCAGCGGAGGCTCTT 2712
Qy 838 uThrAspThrPheAspAlaIleProGlnProAlaArgGlnAlaIlePheAlaSerAsp 858
Db 2713 TGTGACGTGGGCTGGCGCGGCGCGGCGGAGAGTGAAGGCGCGCTGGGC----- 2764
Qy 858 rLeuArgThrGlyArgSerArgSerGlnSerIleCyValAlaGly 874
Db 2765 ---CAGTGACCGCGCGCGGCGCTTCTCAGACGCTGCTCCGAGGT 2809

RESULT 8
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCON POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1

Db	2005	-----ATCCCCCGACAGACCGAGCGCTACTTTGGGGCC	2040
Qy	608	-----GUGInThrSerApTyGInSerProValaAspSerLyAspLeuSerGly	624
Db	2041	AAAGAGCCCGAGCCGCGCCGCGGACCAACAGCCCGGAAGAGACGCGGAG	2091
Qy	625	SerIaGInaSenSerGlyCyLeuSerArgSerThrSerIaIaSenIleSerArgGlyLeu	644
Db	2092	CATGTCGACAGGCACGCGGCTGCAATTCACAAATCGTCCGCTCCAGCAGCTCCACGGGC	2148
Qy	645	GInPheIleLeuThrProAsnGlnPheSerIaGInThrPheTyAlaLeuSerProthr	664
Db	2148	-----	2148
Qy	665	MetHisSerGInaIaThrGInValProIleSerGInSerAspGlySerAlaValaIaIa	684
Db	2148	-----	2148
Qy	685	ThrAsnThrIleAlaAsnGInIleAsnThrAlaProLyAsProAlaIaIaProThrLeu	704
Db	2149	-----CAGAAAGAACTTTCGCGCGCGCCCGCGCGCGCC---CTGTCTC	2187
Qy	705	GInIleProPro-----ProLeuProAlaIleLySHis	715
Db	2188	CAGGTGTCGCGCCCTCCACCTCTCTGCGACGACACAGACCGCGC-CCAGGCGCCAGGCAC	2246
Qy	716	LeuProArg-----ProGluThr-----LeuHis-ProAsnProIaGlyLeuGInG	731
Db	2247	CTCCCCCGTGGGGGAGACACAGCGCTCCCTGTGTCGATCCCGCGCGCTGCGCCACAGAGC	2306
Qy	731	uSerIleSerAspValIaThrCyLeuValaIaSerLySgluAsnValGInValaIaG	751
Db	2307	GTCGCTGTCGCGCTCAGCGCGGCGGCGACACCGCGCGCAGCATGAGTTCCTGCGGACAGAGAA	2366
Qy	751	nSerAsnLeuThrLyS-----AspArgSerMetArgLySerPheAspMetGlyGly	769
Db	2367	CACCCCGGCTGACAGGCCCGCCCGAGAGGGAGACCTCGGGAGACAGC-----GA	2411
Qy	769	uThrLeuLeuSerValCySPrometValProLyAspLeuGlyLySerLeuSerValG	789
Db	2412	CACGTCCATCTCCATCCGCTCCGTGAGACACAGAGAGCTGAGAGCTTCTTCAAGCGGCTT	2471
Qy	789	nasnLeuIleArgSerThrgInGluLeuAsn	799
Db	2472	CAGCATCTCCAGTCCAGTCCAGAGAACTGGAT	2502
RESULT 9			
US-09-105-058C-22			
Sequence 22, Application US/09105058C			
Patent No. 6403360			
GENERAL INFORMATION:			
APPLICANT: Blonar, Michael A.			
APPLICANT: Dworaczky, Steven			
APPLICANT: Gribkoff, Valentin K.			
APPLICANT: Levesque, Paul C.			
APPLICANT: Little, Wayne A.			
APPLICANT: Neubauer, Michael G.			
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME			
FILE REFERENCE: 3053-4052			
CURRENT APPLICATION NUMBER: US/09/105,058C			
CURRENT FILING DATE: 1998-06-26			
PRIOR APPLICATION NUMBER: US 60/055,599			
PRIOR FILING DATE: 1997-08-12			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 22			
LENGTH: 2169			
TYPE: DNA			
ORGANISM: mouse			
US-09-105-058C-22			
Alignment Scores:			

[illegible]

QY	337	AsnLeuIleGlnCysValaITPrpArgSerYrYlaaIlaAsp-----	349
Db	1012	GGTGTGATCCAGTCTGCCTCGGAGATCTTATGTATATACCTTCAACGACCGACCTGCAC	1071
QY	350	-----GlnUysSerValSerIlealaIthrTrpLys-----ProHis	361
Db	1072	TCCACGTGGCAGTACTACAGACGGCAGCTACTCTGCCATGTACAGACTATCCACCT	1131
QY	362	LeuYsaIalaLuhIleThrCys-----	368
Db	1132	CTGAACCAAGCTGGAGCTCTGTAGGAATTCAGACCAATTCGGACTCACTTCAGGAAG	1191
QY	369	-----SerProThrangIlnUysLeuSerPheUysGlnArgValArg	382
Db	1192	GAGCCACACCGACAGACCATACCA---AGTCAGAAAGTCAGTTGAAAGATCGTCTC---	1245
QY	383	MetAlaSerProAlaUyGlnSerIleUysSerArgGlnAlaSerValGlyAsp-----	400
Db	1246	TTCTCCACCCCCCGAGGTGGCTGTCCCAAGGAAAGGAGTCTCCCGACGCCACACGGCTC	1305
QY	401	ArgAlrSerProSerThrAspIleThrAlaGlnUysSerProThrLysValGlnUysSer	420
Db	1306	CGGGGCTCCCCCAGTGGCGGATCAAGCTTTGATGACACCCGAGAAAGTCCCAAGAC	1365
QY	421	TrpSerPheAsnAspArgTThrArgPheArgProSerIleUyGlnUysSerGlnPro	440
Db	1366	TGGAGCTTTGGTGAACCGCAGCCGACACGACGGCTTCCGCATCAAGAGGTGTGCATCC	1425
QY	441	LysProValIleAspAlaAspThrAlaLeuGlnUyThrAspAspValTyAspGlnUysGly	460
Db	1426	CGGCAGAAATTCAGAAACAAAGCTCCCT---GGGAGGACATCTGAGAGACAAACAGAC	1482
QY	461	CysGlnCysAspValSerValGlnAspLeuThrProProLeuUysThrValIleArgAla	480
Db	1483	TGTAACTCCGAGTTGTGACTGAAGATCTTACCTCGCTCAAAAGTTAGCATCAGACT	1542
QY	481	IleArgIleMetUysPheHisValAlaUyArgUysPheUysGlnUyThrLeuArgProArg	500
Db	1543	GTGTGTGTTATAGCGGTCTGTGTATCTTAAGGAAAGTTCAAGAAAGTCTCGGCCATAT	1602
QY	501	AspValUysAspValIleGlnUlnUysSerAlaGlnUysLeuAspMetLeuUysArgIle	520
Db	1603	GATGTGATGACGATCATCGAAACAGTACTCGGCTGGACACTTGATATGTTGCCCGATC	1662
QY	521	LysSerLeuGlnThrArgValAspGlnIleLeuGlnUyGlyGlnIleThrSerAspLys	540
Db	1663	AAGAGCCCGACGTCCAGAGTGACCAAGATTGTGGGCGGGCCCAACAATACGAT---	1719
QY	541	LysSerArgGlnUysIleThrAlaGlnUysIleGlnUyThrTrpAspAspLeuSerMetLeuGly	560
Db	1720	AAGAGATCCACCAAAAGCCACCGAAACGAGACCTGCCGAAAGCCACGACATATATGGGA	1779
QY	561	ArgValValUysValGlnUysGlnValGlnSerIleGlnUySerUyLeuAspCysLeuLeu	580
Db	1780	CGGCTTGGAAAGGTGAGAAACAGAGTCTTGTCATGAAAGAAAGCTGCACTTCTTGGTG	1839
QY	581	AspIleUyTrpGlnGlnValLeuUyArgUysUySerAlaLeuAlaLeuAlaSerPhe	600
Db	1840	AGCATCTATACACAG---AGAAATGGGC-----	1863
QY	601	GlnIleProPheGlnUys-----GlnGlnThrSer	611
Db	1864	---ATCCACACGACGAGACAGAGGCTATTTTGGGCGCCAAAGAGCTGACCCGGACCA	1920
QY	612	AspUyTrpGlnSerProValAspSerUyAspLeuSerGlySerAlaGlnAsnSerGlyCys	631
Db	1921	CCCTACACACAGCCAGAGACAGCCGTAC-----CATGCAGACAAACATGGCGGT	1971
QY	632	-----LeuSerArgSerThrSerAlaAsnIleSerArgGlyUyLeuGlnPheIleUy	648
Db	1972	ATCATTAAGATCGTCCGCTCCACCAAGCTCT-----	2001
QY	649	ThrProAsnGlnPheSerAlaGlnThrPheTyAlaLeuSerProThrMetHisSerIln	668

```

Db      2002 -----ACGGCCACGAGAGACTAGCAGACACCCACGACATC-----CCC 20410
Oy      669 AlathrGlnValProIleSerGlnSer 677
          ||| ||| ||| ||| |||
Db      2041 CCGGCCAGGTGCTCTCCCTCCACCTCG 2067

RESULT 10
US-09-177-650-1
: Sequence 1, Application US/09177650
: Patent No. 6413719
: GENERAL INFORMATION:
: APPLICANT: Leppert, Mark F.
: APPLICANT: Singh, Nanda
: APPLICANT: Chatterjee, Carole
: TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
: TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BRNC)
: FILE REFERENCE: 2323-134
: CURRENT APPLICATION NUMBER: US/09/177,650
: CURRENT FILING DATE: 1998-10-23
: EARLIER APPLICATION NUMBER: 60/063,147
: EARLIER FILING DATE: 1997-10-24
: NUMBER OF SEQ ID NOS: 129
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3232
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (128)..(2743)
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (975)..(976)
: OTHER INFORMATION: There is an insertion of a GT between nucleotides
: OTHER INFORMATION: 975 and 976 in kindred K1504.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (978)
: OTHER INFORMATION: The mutation A to G occurs at this base in kindred
: OTHER INFORMATION: K3904.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (1043)
: OTHER INFORMATION: The mutation G to A occurs at this base in kindred
: OTHER INFORMATION: K1705.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (1691)..(1703)
: OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
: OTHER INFORMATION: deleted in kindred K3369.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (1039)
: OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
: OTHER INFORMATION: the control population.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (1846)
: OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
: OTHER INFORMATION: the control population.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (1469)
: OTHER INFORMATION: The mutation C to T occurs at this base in kindred
: OTHER INFORMATION: K1525.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (1094)
: OTHER INFORMATION: The mutation C to T occurs at this base in kindred
: OTHER INFORMATION: K4443.
: FEATURE:

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Db      892 ACCGTCATTTGGTCTGCTTTGCTCTTCCGGCTGGCATTTTGGGATCCGGCTTTC 951
Qy      317 LeuLeuValGlnGlnGlnIleArgGlnIlePheGlnIleuArgArgPheProAla 336
Db      952 CTGAAGGTCGCAAGACGATCGGCAAAACCTTTGAGAAAGCGGAAACCTTGGCGCA 1011
Qy      337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db      1012 GGTCTATCATCGTCTGGCTGGAGATTCTATGCTACTAACCCTTCACGCCACCCAGCTGCAC 1071
Qy      350 -----GluYSerValSerIleAlaThrTyrProIleuLeuYs 363
Db      1072 TCCACGTGGCAGTACTACGACGACAGTCACTGCTCCCATGTACAGCTCAAACTCAA 1131
Qy      364 -----AlaLeuIleThrCysSerProThrAsnGln----- 373
Db      1132 ACCTATGGGGCTCCAGACTCATCCACTCTGAAACGCTGAGCTGTAGAAATCTTC 1191
Qy      374 -----LysLeuSerPheYsGlnArgValArg-----MetAlaSerPro 386
Db      1192 AAGAGCAATCTGGACTCACCTTCAGAAAGACCCACAGCCAGACCATCACCAAGCCC 1251
Qy      387 ArgGlyGlnSerIleYsSerArgGlnAlaSerValGlyAsp-----ArgArgSerPro 404
Db      1252 CGAGGCGATGGCTGCCAAAGGAGAAAGGGGTCTCCCAAGGCCAGACGGTCCGGCGTCCCC 1311
Qy      405 SerThrAspIleThrAlaGlnGlySerProThrIleValGlnYsSerTyrPheAsn 424
Db      1312 AGGCGGATCAGAGTCTTGATGACACGCCAGAAAGTGCCTCAAGAGCTGGAGACTTTGGT 1371
Qy      425 AspArgThrArgPheArgProSerLeuArgIleYsSerSerGlnProIle 444
Db      1372 GACCGGACGCCGACACGCCAGGCTTCCGATCAAGGAGTCTCATCCCGCAGAAATCA 1431
Qy      445 AspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGlyYsGlnCysAsp 464
Db      1432 GAAGAAGCAAGCTCCCTCGGGAGGACATCGTAGAGCAACAAGAGCTGTAATCGGAG 1491
Qy      465 ValSerValGlnAspLeuThrProProLeuYsThrValIleArgAlaIleArgIleMet 484
Db      1492 TTTGTGACTGAACATCTTACCTCGCTGACCTCAAGTACGACCCGTGTGTATG 1551
Qy      485 LysPheIleValAlaIleYsArgIleYsPheYsGlnIleuArgProTyrAspValYsAsp 504
Db      1552 CGGTTCTTGTAICTAAAGCAAACTTCAAAAGAGAGCTGGCCCAATGATGATGAGCAGC 1611
Qy      505 ValIleGlnGlnTyrSerAlaGlyIleuAspMetLeuCysArgIleYsSerLeuGln 524
Db      1612 GTCATCGAACAGTACTCGGCTGGACACTTGATATGTTGCTCCGCATCAAGAGCTGCAG 1671
Qy      525 ThrArgValAspGlnIleLeuGlyYsGlyGlnIleThrSerAspYsYsSerArgGlu 544
Db      1672 ACCAGAGTGAACAGATTGTGGGGCGGGGCCCAACATTAACGAT---AAGGATCCACCC 1728
Qy      545 LysIleThrAlaGlnIleGlnIleuThrThrAspAspLeuSerMetLeuGlyArgValYs 564
Db      1729 AAGAGCCGACGGAACGAGAGCTGCCGGAAGACCCAGCATGATGAGACCGCTGGGAAG 1788
Qy      565 ValGlnYsGlnValGlnSerIleGlnSerYsLeuAspCysLeuLeuAspIleTyrGln 584
Db      1789 GTGGAGAAACAGAGCTTTGTCATGAGAAAGAGCTGCACTTCTGGTGGACATCTATAACA 1848
Qy      585 GlnValLeuArgIleGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPro 604
Db      1849 CAG-----AGAATGGGATCCCAACGACGACAGACAGAGGCTATTTTGGGGCCAAAG--- 1899
Qy      605 PheGlnCysGlnIleThrSerAspTyrGlnSerProValAspSerIleYsAspLeuSerGly 624
Db      1900 ---GAGCGTGAAGCGGACCAACCTTACCAAGCCAGAGAGACAGCGGTGAC----- 1947
Qy      625 SerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsnIleSer 641
Db      1948 CATGCAGACAAAGCATGGCTGTATCATTAAGATCGTCCGCTCCACGAGCTCTACGG--GCC 2005

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Qy      642 ArgGly-----LeuGlnPheIleuThrProAsnGln 652
Db      2006 AAGGAACTACCGCAGACACCCCAAGCCATCCCTTCGACAGTGTCTCTCTCACTCGT 2065
Qy      653 PheSerAlaGlnThr-----PheTyr 659
Db      2066 GGGCGGACAGCCACGACCGCCATGGACCTCCCTGTGGAGACCATGTGCTACGTGAC 2125
Qy      660 AlaLeuSerProThrMetIleSerGlnAlaThrGlnValProIleSerGlnSerAspGly 679
Db      2126 GCATCCACCACTCTCCCTGCACAGAGCGGTCCGTGTGCT----- 2167
Qy      680 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsn---ThrAlaProIlePro 698
Db      2168 ---ACGTGGGGGCAACAAGACGACGATGTCGAGTCTTGAAGCTGAGAGGCCACCCAGCTT 2224
Qy      699 AlaAlaProThrThrLeu 704
Db      2225 GCAGGCGCTCTGAGGCTG 2242

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RESULT 12

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US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

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Alignment Scores:

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Pred. No.: 4,24e-158 Length: 2565
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: Gaps: 28

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US-09-810-796-5 (1-888) x US-09-105-058C-26 (1-2565)

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Qy      3 AspValGlnSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
Db      91 GACGTGGAGCAA-----GTCACTTGGGGCTCGGGGCGGAGCCGCAAAAGCGGG 141
Qy      22 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgIle 42
Db      142 ACCCTGTCTCTG-----GAGGCGGCGGCGCCGACAGAGGG 177
Qy      43 SerArgArgGlyYsGlnGlyAlaArgMetSerLeuLeuGlyYs---ProLeuSerTyr 61
Db      178 CAGCGGAGGAGACCCCGAGGGC-----ATCGGGCTCTGGCCAAAGACCCCGCTGAGCGC 231
Qy      62 ThrSerSerGlnSerCysArgArgAsnValYsTyrArgArgValGlnAsnTyrIleTyr 81
Db      232 CCAGTCAAG-----AGAAACAAACGCAAGTACCGGCGGATCCAACTTTGATCTAC 282

```

Qy	82	AsnValIleuGluArgProAlaGlyTyrPalaPheIleTyrHisAlaPheValPheIleu	101
Db	283	GAGCCCTCGAGAGAGCCGGGGGCGCTGGCTTTCACAGCGCTTGCTCTGATT	342
Qy	102	ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrIleLeu	121
Db	343	GTCCTGGGGTCTTGATTCTGGCTCTCTGACACACATTCMAAGAGTATGACACTGTCCG	402
Qy	122	SerSerCysLeuLeuIleLeuGluPheValMetIleValPheGlyLeuGluPheIle	141
Db	403	GGAGACTGCTTCTGTACTGTAGAGACATTTGCTATTTTCATCTTTGGAGCGAGTTTCT	462
Qy	142	IleArgIleTyrPheSerAlaGlyCysGlyGlyArgTyrAlaGlyTyrGlnGlyArgLeuArg	161
Db	463	TTTGAGACTGTGGCTGGCTGTGATGTTGTGCGCGATACAAAGCTGGCGGGCGACTGTAG	522
Qy	162	PheAlaArgLysProPheCysValIleAspThrIleValIleuIleAlaSerIleAlaVal	181
Db	523	TTTGCCAGAAAGCCCTGTCATGTGGACATCTTGTGCTGATTGCTCTGTGGCAAGT	582
Qy	182	ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe	201
Db	583	GTTGCTGTGGAAACCAAGGCAATGTTGTGGCACTCC---CTGCGAAGCTGTGGCTTC	639
Qy	202	LeuGlnIleLeuArgMetValArgMetAspArgArgGlyTyrThrTyrPysLeuLeuGly	221
Db	640	CTGCAGATCCCGCGCATGCTCGGATGTGACCGAGAGGTGGCACCTGGACATCTTGAGC	699
Qy	222	SerValValTyrAlaHisSerIleGluLeuIleThrAlaTyrIleAlaGlyPheLeuVal	241
Db	700	TCAAGCATCTGTGCCACAGCAAGAACTTCATCACGGCTGGTACATGGATTCCTGACA	759
Qy	242	LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla-----	256
Db	760	CTCATCTCTTCTTCACTTTCTTGTCACCTGGTGTGAAGAAGCTCCAGAGTGGATGCA	819
Qy	257	-----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyTyr	271
Db	820	CMAAGAGAGGATGAAAGAGAGAGATTGTAGACTTATGACAGATGCGCTGTGGGGCGCTG	879
Qy	272	IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrPheGlyArgLeu	291
Db	880	ATCACTACCTGGCCACCATTTGGCTATGTGAACAAGAACCAACCAACCTGGAAAGCGCTGTG	939
Qy	292	LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeu	311
Db	940	ATTGCGCGCACCTTTCTCTTAATTGGCTCTCTTTTGGCCCTTCAGCGGGCATCTGTG	999
Qy	312	GlySerGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArg	331
Db	1000	GGGTCCGGGCTGGCCCTCAAGGTGCAGAGAACACCGTCGAAGCACTTTGAGAAAGG	1059
Qy	332	ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrPheSerTyrAlaAlaAspGluLys	351
Db	1060	AGGAAGCCAGCTCGAGCTCAATTCAGGCTCGCTGGAGGTATTTATGACCAACCCCAAC	1119
Qy	352	SerValSer---IleAlaThrTyrLys-----ProHisLeu	362
Db	1120	AGGATTGACCTGGTGGCGACATGTGAGATTTATGAATAGTCGTCTTTTCTTCTTC	1179
Qy	363	LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg	382
Db	1180	AGGAAGAAGACGTGGAGGACAGATCCAGCAAAAGCTGGGCTCTTGATCGGGTTCGC	1239
Qy	383	MetAlaSerProAlaGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg	402
Db	1240	CTTTCTAATCTCGGTGAGCAATTAATAA-----GGAAGACTAATT	1281
Qy	403	SerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSerTyrSer	422
Db	1282	ACCCTCTGAATGTAGATGCCATAGACAAAGTCTTTTAAGAACAACAAAGCTGTTGGC	1341
Qy	423	PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys-----	436

Db	1342	TTAAACAATTAAGAGCGTTTCCGACGGCCCTCCGACGAAAGCCTACGCTTTCGGAC	1401
Qy	437	SerSerGlnProPylProValIleAspAlaAspThrAlaLeuGlyThrCysAspValTyr	456
Db	1402	AGTTCTGAA-----GATCCGGGACAGGT-----GACCCCATGGCG	1437
Qy	457	AspGluValSerGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuValThr	476
Db	1438	GAAACACAGGGGCTATGGGAATGACTTCCCTCCACAAAGCATGATCCCACTGAAGGCC	1497
Qy	477	ValIleAspAlaIleArgIleMetLeuPheHisValAlaValAspGlyLeuPheGlySerIle	496
Db	1498	GCCATCCGAGCGGTGAGATTCTCAATTCGCTCTATATAAAAAAATTCAAGAGACT	1557
Qy	497	LeuArgProTyrAspValIleAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet	516
Db	1558	TTGAGCGCTTACGATGTGAGATGTGATTAAGCAGTATTTCTCCGGGCACTCGACATG	1617
Qy	517	LeuCysArgIleLeuSerLeuGlnThrArgValAspGlnIleLeuGlyValGlyGlnIle	536
Db	1618	CTTTCACGAGATAAAGTACTTCACAGCAGATAGATGATTTTACCCCTGACCTCC	1677
Qy	537	ThrSerAspIleValSerArg-----	543
Db	1678	TCCACGCCAAACACAAAGAGTCTCAGAAAGGTGACGATTCACCTTCCATCCAGCAA	1737
Qy	544	-----GluTyrIleThrAlaGluHisGlnThr-----AspAspLeuSer	557
Db	1738	TCTCCACGAGATGAACCATATGTACCCAGACCATTCACATCAGAAATGGAACCAAAAC	1797
Qy	558	MetLeuGlyArgValValIleValGluValGluValGlnSerIleGluSerLeuAsp	577
Db	1798	ATGATGGGGAGATTGTGTAAGATTGTAAGAACAGGTTCAGACATCGGAGAAAGAGCTGAC	1857
Qy	578	CysLeuLeuAspIleTyrGlnGlnValLeuArg-----	588
Db	1858	TTCTCTCGGATATGACATGCACATGCACATGGAACCGTTGCAGTGCAGTACGAGATAT	1917
Qy	589	-----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPhe	605
Db	1918	TACCAACCAAGGGGACTCTCTCG-----CCAGCT	1947
Qy	606	GluCysGlnGlnThrSerAspTyrGlnSerProValAspSerIleAspLeuSerGlySer	625
Db	1948	GAGCAGAGAGAAAGAGAGACAAACAGGATTCG---GATTGGAATAACATCATCTGCACAC	2004
Qy	626	AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln	645
Db	2005	TATTCGAGACAGGCCCCCGGAAACCACTTACAGCTTCCAC-----	2046
Qy	646	PheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet	665
Db	2047	---CAGGAGACCATTTGACAAAGTACGCCCTATGGGTTTTTGCCATGACCTT-----	2097
Qy	666	HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThr	685
Db	2098	-----GNGAACCTGCCCCGAGGGGACCCAGTTCGGAAAGGTTCAAGCAACT	2145
Qy	686	AsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGln	705
Db	2146	-----CTCTCTTCTCAGCAACAACTGATGTGAG	2175
Qy	706	IleProProLeuProAlaIleLeuHisIleLeuProArgProGluThrLeuHisIleProAsn	725
Db	2176	AGGCCCAAGCTCTGCTTATCTTTCATCTTTCGACCTCCGAGTGAAGGTGGCAC---TCC	2233
Qy	726	ProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLeuGlu	745
Db	2233	CAGCTGACCTGCAAGGGCCCTACTCGAC-----	2266
Qy	746	AsnValGlnValAlaGlnSerAsnLeuThrIleAspArgSerMetArgLeuSerPheAsp	765

Db 2263 CGATATCCCCCGGAG-----AGACCTAGCATCAG 2295
Qy 766 MetGlyGlyIuThrLeuSerValCysProMetValProIysAspLeuGlyLysSer 785
Db 2296 CGAGACGATACACACTCTGTCTCTG----- 2322
Qy 786 LeuSerValGlnLeuLeuIleArgSerThrGluLeuLeuIleGlnLeuSerGlySer 805
Db 2323 ATGCGGTCAACAC-----GAGAGCTGAGAGAGCTCTCCAACTGCGCTTC 2367
Qy 806 GluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTyrArg 821
Db 2368 AGCATCTCCCGAGACAGATGATGATGATGTCGCGCCCAATGCGGCGTGCAGCTGGATG 2427
Qy 822 GluSerIleuPheIleThrAspGluValGlyProGluGluIuThrGluIuThrAspThr 841
Db 2428 AGGAGAGCGGCTACTCTGCGCGAG-----GCTGAGACGACACAGACGAGACCCC 2478
Qy 842 Phe 842
Db 2479 TTC 2481
RESULT 13
US-09-177-650-6
Sequence 6, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BNPC)
TITLE OF INVENTION: AND OTHER EPILEPTSES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2914
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(2634)
FEATURE:
NAME/KEY: allele
LOCATION: (840)
OTHER INFORMATION: The polymorphism of a T to a C at this position
OTHER INFORMATION: has appeared in one individual.
FEATURE:
NAME/KEY: mutation
LOCATION: (947)
OTHER INFORMATION: The missense mutation from a G to a T occurs at
OTHER INFORMATION: this position in a BNPC family.
FEATURE:
NAME/KEY: allele
LOCATION: (678)
OTHER INFORMATION: This position is polymorphic for C or T.
FEATURE:
NAME/KEY: allele
LOCATION: (750)
OTHER INFORMATION: This position is polymorphic for T or C.
FEATURE:
NAME/KEY: allele
LOCATION: (1089)
OTHER INFORMATION: This position is polymorphic for G or C.
FEATURE:
NAME/KEY: allele
LOCATION: (2598)
OTHER INFORMATION: This position is polymorphic for T or C.

US-09-177-650-6
Alignment Scores:
Pred. No.: 5,37e-158 Length: 2914
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: 3 Gaps: 28
US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)
Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaIleArgIleAspGly 22
Db 163 GACGTGAGCA-----GTCACCTTGCGCCTCGGGGCGGACCGACCAAGACGG 213
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 214 ACCCTGCTGCTG-----GAGGCGGCGGCGCGAGAGG 249
Qy 43 SerArgArgGlyArgGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 250 CAGCGGAGAGACCCCGAGGAC-----ATCGGCTCTGCGCCAAAGACCCCGTGCAGCCGC 303
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 304 CCAGTCAAG-----AGAAACAAGCCCAAGTACCGGCGCATCCAACTTGATCTAC 354
Qy 82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 355 GAGCGCTGAGAGACCGCGGCGCTGGCGCTTACCAACGCTGGTGTCTGAT 414
Qy 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
Db 415 GTCTCGGGGTCTGATGCTGCTGCTGCACCATTCACAGAGATAGAGACTGCTCG 474
Qy 122 SerSerCysLeuLeuLeuGluPheValMetIleValAlaPheGlyLeuGluPheIle 141
Db 475 GGAAGCTGCTTCTGTACTGAGAGACATTTGCAATTTTCATCTTTGAGCCGAGTTTGC 554
Qy 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPngIuArgLeuArg 161
Db 535 TTGAGGATCTGGGCTGCTGATGTTGCTGCCGATCAAGAGCTGCGGCGCCAGTGAAG 594
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 595 TTGGCCAGAGAGCCCTGTGCATGTTGACATCTTGTGCTGATTCCTGTGCGCAGTG 654
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 655 GTTGTCTGGGAAACCAAGCAATGTTCTGGCCACTTC---CTGCAAGCCCTGCGCTTC 711
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyIleThrTrpLysLeuLeuGly 221
Db 712 CTGCAGATCTCGGCGATGCTGGAGTACCGGAGAGTGCACCTGGAAGCTTCTGGGC 771
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db 772 TCAGGCATCTGTGCCACAGCAAAAGATCATTCACGCGCTGTGACATCGGTTCTTCGACA 831
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
Db 832 CTCATCTTTCTTCATTTCTTCTGCTACCTGTTGAGAAAGACGTCCTCCAGAGTGATGCA 891
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271
Db 892 CAAGAGAGAGATGAAGAGAGATTGAGACTATGACAGATGCCCTGTGTGGGCGCTGC 951
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291
Db 952 ATCACACTGCGCCACATTTGCTATGAGACCAAGACCCCAAAACGTTGGAGGCGCTCTCG 1011
Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeu 311

Db 1012 ATTCGCGCACCTTTCTTAATTCGCTCTTTTTCGCTTCACGCGGCATCTCG 1071
Qy 312 GYSeRgLYPheALeuLYsValGInGluGlnHISarGInLYshISpHeGInLYsArG 331
Db 1072 GGGTCGGGGCTGGCCCTTCAGAGTCGACGACCAACCGTCAGACGATTTGAGAAAAG 1131
Qy 332 ArgAsnProALaALaAsnLeuIleGInCYsValTTPArGSeTYrALaALaAspGInLYs 351
Db 1132 AGGAACCCAGCTGCTAGCTCATTCAGGCTGCTGAGGATATATGCTACCAACCCCAAC 1191
Qy 352 SerValSer---IleAlaThrTrpLYs-----ProHISLeu 362
Db 1192 AGGATTGACCTGGTGGACATGGAGATTTTATGAATCAGTCGCTCTTTTCTTTCTTC 1251
Qy 363 LYsAlaLeuHISThrCYsSerProThrAsnGInLYsLeuSerPheLYsGInArGValArG 382
Db 1252 AGGAAGAAACAGCTGGAGGACGATCCAGCAAAAGCTGGCTCTTGGATCGGGTTCCG 1311
Qy 383 MetAlaSerProArGInLYsInSerIleLYsSerArGInAlaSerValGInLYsArGArG 402
Db 1312 CTTCCTAATCTCGTGGTAGCAATACCTAAA-----GGAAAGCTATTT 1353
Qy 403 SerProSerThrArGInLYsThrAlaGInLYsSerProThrLYsValGInLYsSerTrpSer 422
Db 1354 ACCCTCTGAATGTAGATGCCATAGAAAGAGCTCTTAAAGAACCAAAAGCTGTGGC 1413
Qy 423 PheAsnArGInLYsThrArGArGProSerLeuArGLeuLYs----- 436
Db 1414 TTAAACAATTAAGAGGCTTTCCGACGGCTTCGCGATGAAGACCTACCGCTTCTGGCAG 1473
Qy 437 SerSerGInProLYsProValIleAspAlaAspThrAlaLeuGInLYsThrArGArGValTYr 456
Db 1474 AGTTCTGAA-----GATGCCGGAGCAGGT-----GACCCCAAGCGG 1509
Qy 457 AspGInLYsGInLYsGInCYsAspLYsAspValSerValGInAspLeuThrProProLeuLYsThr 476
Db 1510 GAAGACAGGGGCTATGGGAATGACTTCCCATGAAAGACATGATCCCATCGTGAAGGCC 1569
Qy 477 ValIleArGAlaIleArGIIleMeLYsPheHISValAlaLYsArGInLYsPheLYsGInLYsThr 496
Db 1570 GCATCTCGAGCGCTCGAATTCACAAATCCGCTCTATTAATAAAATATTCAGAGAGACT 1629
Qy 497 LeuArGProTYrArGValLYsAspValIleGInGInLYsSerAlaGInLYsLeuArGMet 516
Db 1630 TTGAGGCTTACCATGTGAAGGATGTGATTCAGACATATTCGCGGACATCTCGACATG 1689
Qy 517 LeuCYsArGIIleLYsSerLeuGInThrArGValAspGInIleLeuGInLYsGInIle 536
Db 1690 CTTCACGATTAAGTACCTTCAGACGAGATAGATATTTTCACCCCGGACTCCC 1749
Qy 537 ThISerAspLYsLYsSerArG----- 543
Db 1750 TCCAGCCCAAAACACAAAGAGTCTGAAGAAAGGTCAAGATTCATCCCATCCCAAGAA 1809
Qy 544 -----GInLYsIleThrAlaGInHISGInThr-----AspAspLeuSer 557
Db 1810 TCTCCAGAGATGAAACCATATGTAGTCAGACCATTCACATCAAGAAATCCAAAGCCAAAG 1869
Qy 558 MetLeuGInLYsValValLYsValGInLYsGInValGInSerIleGInLeuSerLYsLeuArG 577
Db 1870 ATGATGGGAGAGTTTGTAAAGTTGAAGACAGGTTTCAGACATGGGGAAAGAGCTGAGC 1929
Qy 578 CYsLeuLeuAspIleTYrGInGInValLeuArG----- 588
Db 1930 TTCTCTGTGATATGACATGCACAAACATGAAACGATTGCAAGTGCAGGTCACGAGATAT 1989
Qy 589 -----LYsGInSerAlaSerAlaLeuAlaLeuAlaSerPheGInIleProPhe 605
Db 1990 TACCCAACCAAGGGCAGCTCTCG-----CCAGCT 2019
Qy 606 GInCYsGInGInThISerAspTYrGInSerProValAspSerLYsAspLeuSerGInLYsSer 625

Db 2020 GAAGCAGAGAAAGAGAGACACAGTATTC-----GATTGAAAACCATCATCTTCGAAC 2076
Qy 626 AlaGInAsnSerGInCYsLeuSerArGSerThISerAlaAsnIleSerArGInLYsLeuGIn 645
Db 2077 TATTCGAGACAGGCGCCCGGAACCAACCTACACACTTCAC----- 2118
Qy 646 PheIleLeuThrProAsnGInPheSerAlaGInThrPheTYrAlaLeuSerProThrMet 665
Db 2119 ---CAGGTGACCATTCAGCAAAAGTCAAGCCCTATGGGTTTTTGGACATGACCT----- 2169
Qy 666 HISserGInAlaThrGInValProIleSerGInSerAspGInSerAlaValAlaIleThr 685
Db 2170 -----GTAAACCTGCGCCGAGGGGAGACCACTTCGGAAGGTTGAGGCAACT 2217
Qy 686 AsnThrIleAlaAsnGInIleAsnThrAlaProLYsProAlaAlaProThrThreGIn 705
Db 2218 -----CCTCTCTCTCAGCAAAACGATATGGAG 2247
Qy 706 IleProProProLeuProAlaIleLYsHISLeuProArGProGInThrLeuHISProAsn 725
Db 2248 AGGCGCACGGTCTGCTATCTTGACTCTTCGACTCCGAGTGAGCTGCCAC--TCC 2304
Qy 726 ProAlaGInLYsLeuGInGInSerIleSerAspValThrThrCYsLeuValAlaSerLYsGIn 745
Db 2305 CAGGCTGACCTGCAGAGGCCCTACTCGAG----- 2334
Qy 746 AsnValGInValAlaGInSerAsnLeuThrLYsAspArGSerMetArGInLYsSerPheAsp 765
Db 2335 CGAATCTCCCCCGGACAG-----AGACGTAGCATTCACG 2367
Qy 766 MetGInLYsGInThrLeuLeuSerValCYsProMetValProLYsAspLeuGInLYsSer 785
Db 2368 CGAGACAGTGACACACTCTGCTCGT----- 2394
Qy 786 LeuSerValGInAspLeuIleArGSerThrGInGInLeuAsnIleGInLeuSerGInLYsSer 805
Db 2395 ATGTGCTCAACAC-----GAGAGCTGAGAGAGCTTCACAGTGGCTTC 2439
Qy 806 GInSerSerGInLYsSerArGInLYsSerGInAspPheTYrPro-----LYsTPArG 821
Db 2440 AGCATCTCCAGGACAGAGATGATATGTTGGCCCCCAATGGGGGTGAGCTGAGATG 2499
Qy 822 GInSerLYsLeuPheIleThrAspGInGInValGInLYsProGInGInThrGInThrAspThr 841
Db 2500 AGGGAAGCGGATCTCGCGAG-----GGTGAGCGAGACACAGACCGACCC 2550
Qy 842 Phe 842
Db 2551 TTC 2553

RESULT 14
US-09-177-650-90
Sequence 90, Application US/09177650
Parent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCMO2 AND KCMO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
LENGTH: 2814
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (202) ... (2811)
US-09-177-650-90

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Score: 1550.50 Matches: 382
Percent Similarity: 54.43% Conservative: 109
Best Local Similarity: 42.35% Mismatches: 245
Query Match: 34.10% Indels: 167
DB: 3 Gaps: 27

US-09-810-796-5 (1-888) x US-09-177-650-90 (1-2814)

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DB 340 GAGGTGAGAGAA-----GTCACTTGCGCTAGGGCCGAGCGCAAAAGCGGG 390
QY 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGly 42
DB 391 ACCCTGCTGCTG-----GAGGCGGTGGCCCGCAAGAGCGG 426
QY 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
DB 427 CAGAGAGAGACCCCGCAGGCG-----ATCGGCTCTGGCAAAAGACCCCTGAGCGCG 480
QY 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
DB 481 CCAGTCAAG-----AGGAACAAACGCCAAGTACAGCGCATCCAACTTTGATCTAT 531
QY 82 AsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
DB 532 GAGCGCTGAGAGACCGCGGGCTGGCGCTGCTCTACACCGCTGTGTTCTTGAT 591
QY 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeuAla 121
DB 592 GTCTCGGAGATGCTGATTTCTGGCGCTGCTCACACCTTCAAGAAATATGAGACTGTGCT 651
QY 122 SerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLeuGlnPheIle 141
DB 652 GGAAGCTGCTTTTGTGCTGCGAAACATTTGCTATTTTCCTTTGAGCTGAGTTGCT 711
QY 142 IleArgIleTyrPserIleGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeuArg 161
DB 712 TTGAGAGATCTGGGCTGAGAGATGTTGCTGCTGATACAAAGCGTGGCGCTGAAG 771
QY 162 PheAlaArgLysProPheCysValIleAspThrIleValIleuIleAlaSerIleAlaVal 181
DB 772 TTTCAGAGAAAGCCCTGCTGATGTCATCTTGATGATGCTGCTGTCAGT 831
QY 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerIleuArgPhe 201
DB 832 GTTGGCGTGGAAACCAAGGCAATGCTTGGCCACCTCC---CTGGCAACCTTCCTTC 888
QY 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrTyrPheLeuGly 221
DB 889 CTCGACATCTCGGCTGCTGCTTCGAATGATAGAGGGGTGGCACCTGGAAAGCTCTGGGC 948
QY 222 SerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeuVal 241
DB 949 TCGGCTATCTGCTCCCAACAAAGAACTCATCTGCTGTAACATAGAGCTTCTTGACA 1008
QY 242 LeuIlePheSerSerPheLeuValTyrLeuValGlnLysAspAla----- 256
DB 1009 CTCATCTTCTTCATTTCTTGTCTGCTGAGAGAGATGTCGCAAAATGATGCC 1068
QY 257 -----AsnLysGlnPheSerThrTyrAlaAspAlaLeuTyrPheGlyTyr 271
DB 1069 CAAAGAGAGAGATGAAGAGAGATTGAGACTATGCAATGCTCTGTGTGGGCGCTG 1128
QY 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrPheGlyArgLeu 291
DB 1129 ATCACAGTGGCCACCATTTGTTATGAGACRAGACACTTAAACCTGGAGAAAGACGTCTG 1188

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QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeu 311
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QY 312 GlySerGlyPheAlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArg 331
DB 1249 GGTCTAGGACTGGGCACTGAAGGTTTGGAGAGACACCGTCAGAAAGCACTTGGAGAGAG 1308
QY 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGlyLys 351
DB 1309 AGGAAGCCAGCTGGGAGACTATCCAGGCTGCTGAGATATTATGCTACCAACCCCAAC 1368
QY 352 SerValSer---IleAlaThrTyrLys-----ProHisLeu 362
DB 1369 AGGTGGATCTGGTGGCAACCTGGAGATGTTATGAATCAGTTGTCTTTCCATCTTC 1428
QY 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGlnArgValArg 382
DB 1429 AGGAAGAAACAACCTGAGACAGACAGCCAAAGCTGGTCTTGGATCGGTTCCG 1488
QY 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArg 402
DB 1489 CTTTCTAATCTCTGCTGTAACAATACTAA-----GGAAGCTATATT 1530
QY 403 SerProSerThrAspIleThrAlaGlnLysSerProThrLysValGlnLysSerTyrPser 422
DB 1531 ACCCTCTGAATGTAATGCCATAGAAAGCCCTTCCAAAGGCCAAAGCTGTGGC 1590
QY 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer----- 437
DB 1591 TTAACAATAAAGAGGTTTCCGACCGCTTCGAGTAAAGCTTACCTTCTGGCAG 1650
QY 438 ---SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
DB 1651 AGTCTCGAA-----GATGCTGGAGACGCG-----GACCCCAAGGCA 1686
QY 457 AspGlyLysGlyCysGlnCysAspValSerValGlnAspLysThrProProLeuLysThr 476
DB 1687 GAAGACAGGGGCTATGAGGAATGACCTTCATTTGAAAGACATGATCCCTCCAAAGGCT 1746
QY 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThr 496
DB 1747 GCATCCGAGCTGTGAGATTTCTACAGTTCCGCTATATAAAAGTTCAAGAGAGAG 1806
QY 497 LeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAlaGlyHisLeuAspMet 516
DB 1807 TTGAGGCTTATGATGTGAAGATGATGATGAGCATATTGCGCGGACATCTTGACATG 1866
QY 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
DB 1867 CTTTCCAGATTAAGTACTTACAGACAAATAGATATGATTTTCAACCCCTGAGCTCCA 1926
QY 537 ThrSerAspLys---LysSerArgGlnLysIleThr----- 547
DB 1927 TCCACTCCAAACATTAAGAGCTCAGAAAGGAGACGATTTACCTACCATCCAGCAG 1986
QY 548 -----AlaGlnHisGlnThrThrAspAspLeuSer 557
DB 1987 TCTCCAAAGATGAACCATATGTAGCCAGAGGAGCCATCCAGAACTGAAACCAAGC 2046
QY 558 MetLeuLysArgValValLysValGlnLysGlnValGlnSerIleGlnLysSerLysAsp 577
DB 2047 ATGATGGGAGAGTTTGTAAAGATTGAAGACAGGTTTCATGACATGGGAGAAACTGGAC 2106
QY 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
DB 2107 TTCCTGTGAGACATGATGACGATATGAAACGCTTACAGTACATGCTACAGTAC 2166
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605
DB 2167 TACCAACTTAAGGGGCTCTCC-----CCAGCC 2196

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QY 606 GtUcYgEgInThSerApTyrgInSerProValAspSerIysAspLeu-SerGlySe 625
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Db 2197 GAAGGGAGAGAGAGAGAGAGAGTACTT---GATTGAAAACCATCATCTGCAC 2253
QY 625 rAlaGInanSerGlyCyLeuSerArgSerThrSerIAsnIleSerArgIyLeu 645
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Db 2254 TACTCAGAGACAGGGCCCTGACCTCTTACAGCTTCACACGAGTGCCTACGAC 2313
QY 645 nPheIleLeuThrProAsnGluPheSerIAsnThrPheTyraIAspSerPro 665
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Db 2314 GTTGGCCCTTACGGC-----TTTTTGCACATGATCT----- 2346
QY 665 thISerGInAlaThGInValProIleSerGInSerAspGlySerAlaAla 685
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Db 2347 -----GTGAACCTGACCCGAGGGGAGCCAGCTTCAAAAGGCTCA 2387
QY 685 rAnThrIleAlaAsnGInIleAsnThrAlaProIySProAlaAlaProTh 705
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Db 2388 AGCTAACCTTCCCTCC-----TCGGGAAGTACATATGACAGA 2423
QY 705 nIleProProProLeuProAlaIleIyShISeuProArgProGluThrLeu 725
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Db 2424 GAGGCCACAGTCTGCTGCTGATCTGATGATGATGATGATGATGATGATGAT 2478
QY 725 nProAlaGlyLeuGInGluSerIleSerAspValThrThySLeuValAla 745
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Db 2479 -----TCCACAGAC 2486
QY 745 uAnValGInValAlaGInSerAsnLeuThrIySaPArgSerMetArgIySe 765
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Db 2487 AGAAGCTGCAAGGCTCTTATTCGACCAATCTGCCCCCG---CAGAGAGG 2543
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Db 2572 -ATGTCCTGCAATCAC-----GAGGAACCTGAGCGGCTCTCAAGTGG 2615
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RESULT 15
US-09-105-058C-5
; Sequence 5, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blauar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
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; LENGTH: 900
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

Alignment Scores:
Pred. No.: 1,966-118 Length: 900
Score: 1207.50 Matches: 227
Percent Similarity: 83.88% Conservative: 28
Best Local Similarity: 74.67% Mismatches: 40
Query Match: 26,56% Indels: 9
DB: 3 Gaps: 2

US-09-810-796-5 (1-888) x US-09-105-058C-5 (1-900)

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QY 76 ValGInAsnTyrrLeuTyrrAsnValLeuGluArgProArgGlyTyrrAlaPhe 95
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Db 49 CTGCAGAATTCTCTTACACGCTGCTAGAGCGGCCCGCGCTGGCGTTCACTCAC 108
QY 96 AlaPheValPheLeuLeuValPheGlyCySLeuIleLeuSerValPheSerThr 115
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 109 GCTACAGTGTCTCTTGTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 168
QY 116 GtUthrIySLeuAlaSerSerCySLeuLeuIleLeuGluPheValMetIleVal 135
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Db 169 GAGTACGAGAAAGCTCTGAGGGGCGCTTACATCTGGAATGCTATCGTGTGA 228
QY 136 PheGlyLeuGluPheIleIleArgIleTyrrSerAlaGlyCySLeuArgTyrr 155
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QY 156 TrpGInGlyArgLeuArgPheAlaArgIySPProPheCySValIleAspThrI 175
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QY 176 IleAlaSerIleAlaValSerIleAlaSerIleArgInGluAsnIlePheAla 195
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Db 349 ATTGCTTCATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408
QY 196 LeuArgSerLeuArgPheLeuGInIleLeuArgMetValArgMetAspArgGly 215
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QY 216 ThrTrpIySLeuLeuGlySerValValIyrrAlaHisSerIySLeuIleTh 235
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Db 469 ACCTGGAAGCTCTTGGAGATCGGTAGTCAAGCTCAACAGAGAGAGCTGCTGG 528
QY 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuVal 255
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Db 529 TACATGTGCTTCTCTGCTCACTGCTGCTTATCTGCTGCTGCTGCTGCTGCT 588
QY 256 AlaLeuIySLeuPheSerThrTyrrAlaAspAlaLeuTyrrGlyThrIleTh 275
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Db 589 GAGATGACCACTTTGACACCTAGCAGATGACCTGTGGGGCTGATACCTGAGC 648
QY 276 ThrIleGlyTyrrGlyAspIySerThrProLeuThrTrpLeuGlyArgLeu 295
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Db 649 ACCATTGGCTACGGGGAGACAGTACCTGAGACCTGGAACGGGAGGCTCTGG 708
QY 296 PheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGly 315
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Db 769 GCCCTGAAGTCCAGAGACAGATCGGCAAAACCTTTGAGAAACGGGAGAACCT 828
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Qy	336	AlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluIlySerValSerIle	355
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Qy	356	---AlaThrTrp	358
Db	889	CACTCCACGTGG	900

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Job time : 340 secs

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OM protein - nucleic search, using frame_p2n model

Run on: October 23, 2005, 18:01:06 ; Search time 1087 Seconds

(without alignments)
6738.945 Million cell updates/sec

Title: US-09-810-796-5

Sequence: 1 MKDVESGRGVLLNSAARG.....SICKAGESTDALSLPHVKLK 888

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Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS-human40.csi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4547	100.0	2772	9 US-09-825-147-1	Sequence 1, Appli
3	4547	100.0	2772	19 US-10-803-268-1	Sequence 1, Appli
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7	4527.5	99.6	2694	9 US-09-810-796-2	Sequence 2, Appli
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45	1604	35.3	1878	20 US-10-744-796-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: KNOX, a No. US20020102677A1et Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3

LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Alignment Scores:
Pred. No.: 0 Length: 2667
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
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; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
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; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-1

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Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
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Db 1546 ATCAGAAATTATGAAATTTTCATGTTGCAAAACGGAATTTAAAGAAACATTAGCTCATAT 1605
Qy 501 AspValLysAspValIleGlnGlnTyrSerAlaGlyHISLeuAspMetLeuCysArgIle 520
Db 1606 GATGTAAAGATGTCTTGAACAAATTTCTGCTGATCATCTGGACATGTTGTGAAATT 1665
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTGAAAAGGGCAATTCATCAGATAG 1725
Qy 541 LysSerArgGlyLysIleThrAlaGlnHISGlnThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCGGAGAGAAATTAACAGACAAACATGAGAACACAGATCTCAGTATGCTCGGT 1785
Qy 561 ArgValValLysValGlyLysGlnValGlnSerlIeGlySerLysLeuAspCysLeuLeu 580
Db 1786 CCGGTGTGTAAGGTTGAAAACAGATACAGTCCATGAAATCCAAAGTGGAGCTCTACTCA 1845
Qy 581 AapIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1846 GACATCTATCAACAGAGCTCTTGGAAAGGCTGTGCTCAGCCCTCGCTTGGCTCATTC 1905
Qy 601 GlnIleProProPheGlyCysGlnGlnThrSerAspTyrGlnSerProValAlaSerLys 620
Db 1906 CAGATCCCACTTTTAATGTGAACAGACATGATATCAAAAGCCCTGTGATGACAAA 1965
Qy 621 AapLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaLeuIle 640
Db 1966 GATCTTTCGGGTTCCGCAAAAACAGTGGCTGTATCCAGATCAACTGATGCCAAACATC 2025

Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAla 660
Db 2026 TCGAAGAGCGCTGAGTTTCAATCTGACGCGCAATGAGTTCAAGTGGCCACAGCTTCTCAAGCG 2085
Qy 661 LeuSerProThraMetHISerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2086 CTTAGCCCTACTATGACAGTCAAGCAACACAGGGGCCAAATTTAGTCAAAAGCGATGGCTCA 2145
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2146 GCAGTGGAGCCACCAACACATTTGCMAACCAATTAATAGCGACCCAAAGCCAGCAGCC 2205
Qy 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHISLeuProArgProGlu 720
Db 2206 CCAACAACCTTAAACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265
Qy 721 ThrLeuHISProAsnProAlaGlyLeuGlnGlnSerlIeSerAspValThrThrCysLeu 740
Db 2266 ACTTGCAACCCCTAACCCCTGACAGGCTTACAGAAAGCATTTCTGACGTACCACTGCTCT 2325
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Db 2326 GTTGCCCTCAAGAAATGTTTCAGGTTGACAGTCAATTCACCAAGAACCGTTCTATG 2385
Qy 761 ArgLysSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGAATAACCTTTGACATGGAGAGAAACTCGTTGTCTGCTGCTGCCATGGTCCGAAG 2445
Qy 781 AapLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGlnLeuAsnIle 800
Db 2446 GACTTGGGCAAACTTTTCTGTGTGCAAAACCTGATCAGGTGACCGAGAACTGAATATA 2505
Qy 801 GlnLeuSerGlySerGlnSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
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Qy 821 ArgGlnSerLysLeuPheIleThrAspGlnGlnValGlyProGlnGlnThrGlnThrAsp 840
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Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTGATGGCGCACCCGACCTGGCAGGAAAGCTGCTTGTGATCAGACTCTTAAAGG 2685
Qy 861 ThrGlyArgSerArgSerSerGlnSerlIeCysLysAlaGlyGlnSerThrAspAlaLeu 880
Db 2686 ACTGGAAGTCAACATCATCTCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2745
Qy 881 SerLeuProHISValLysLeuLys 888
Db 2746 AGCTTGCCCTCATGTCAAACTGAAA 2769

RESULT 3
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255

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/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2772
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-803-268-1

Alignment Scores:
Pred. No.: 0          Length: 2772
Score: 4547.00       Matches: 888
Best Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19              Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-1 (1-2772)
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QY      21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB      166 GACGGCCTGACTGCTGGGACCCGCGCGCCAGCGCTCGGTGGCGGGGCGGCTG 225
QY      41 ArgGluSerArgArgGlyLyArgGlyAlaArgMetSerLeuLeuGlyLyProLeuSer 60
DB      226 AGGAGAGCGCGCGGGCGAGAGGGGGCCGGATGAGCTGCTGGGGAAAGCCGCTCT 285
QY      61 TyThrSerSerGlnSerCysArgArgAsnValIleThrArgArgValGlnAsnTyLeu 80
DB      286 TACACGAGTAGCCAGAGCTCCGCGCCAGCTCAAGTACCGCGGGGTGCGAACTACCTG 345
QY      81 TyAsnValIleuGluIuArgProArgGlyTTPAlaPheIleTyRhiSaIaPheValPheLeu 100
DB      346 TACAACTGCTGGAGAGACCCCGGGCTGGCGCTTCATCAACACGCTTCGTTTTCTC 405
QY      101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluIuIsthrLyLeu 120
DB      406 CTTCGCTTGGTGGTGGATTTGTGTCAGTGTTCATCCATCCCTCGAGCACACAAATTTG 465
QY      121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB      466 GCCTCAAGTTCCTCTTGAATCCTCGAGTTCGTATGATTTCTCTTTGGTTGGAGTTC 525
QY      141 IleIleArgIleTTPSerAlaGlyCysCysArgTyrArgGlyTTPGlnGlyArgLeu 160
DB      526 ATCATTCGAATCTGCTCGCGGGTGTGTGATATAGAGATGAGGAGAGAGACTG 585
QY      161 ArgPheAlaArgLyProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB      586 AGGTTTGCTCGAAGCCCTTCGTGTATAGATACCATTTCTTCCTTCCTCAATAGCA 645
QY      181 ValValSerAlaIuArgThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB      646 GTTGTTCCTCAAAACTCAGGGTAAATATTTTTCACGCTCGACTCAGAAATCTCCGT 705
QY      201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyIuThrTTPLyLeuLeu 220
DB      706 TTCCTACAGATCCCGCATGTCGCGCATGACGAAAGGGGAGGCACTTGGAATTAACG 765
QY      221 GlySerValValIuArgIleAspSerLyGluLeuIleThrAlaTTPLyIleGlyPheLeu 240
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QY      241 ValIleuIlePheSerSerPheLeuValTyrLeuValGluIuAspAlaLeuLySGluPhe 260
DB      826 GTTCTTAATTTTTCGCTTCCTTCTGTCTATCTGCTGAAAAGATGCGCAATTAAGAGTTT 885
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DB      |||
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DB      886 TCTACATATGAGATGCTCTGTGTGGGCGACAAATTATCATGAACTATGGCTATGGA 945
QY      281 AspLySerThrProLeuThrTTPLeuGlyArgGluLeuSerAlaGlyPheAlaLeuLeuGly 300
DB      946 GACAAAACCTCCCTTAACCTTGCGGGAGATGCTTTCGACAGGCTTTCACCTCTGGGC 1005
QY      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLyValGln 320
DB      1006 ATTTCTTTCTTTGCACTTCCTCGCGCATTTCTTGCTCAGGTTTTCATTAAGATACA 1065
QY      321 GluGlnHisArgGlnLyHisPheGluLyArgArgAsnProAlaAlaAsnLeuIleGln 340
DB      1066 GAACAACACCGCGCAGAAACATTTTGAAAAGAGAACCCAGCTGCACCACTCATTTAG 1125
QY      341 CysValTTPArgSerTyrAlaIleAspGlyLySerValSerIleSaIaThrTTPLyPro 360
DB      1126 TGTGTTGGCGTATGATTAACGACCTGATGGAATCTGTTCCATTGCAACTCGAAGGCCA 1185
QY      361 HisLeuLyAlaLeuHisThrCysSerProThrAsnGlnLyLeuSerPheLySGluArg 380
DB      1186 CACTTGAAGCCTTGACACCTGCACTGCACTTACCAATCAGAACTAATTTAAGAGCGCA 1245
QY      381 ValArgMetAlaSerProArgGlyGlnSerIleLySerArgGlnAlaSerValGlyAsp 400
DB      1246 GTGCGCATGGCTTAAGCCCGAGGAGGAGAGTATTAAGAGCGCAAGCCTCAGTAGGTGAC 1305
QY      401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLyValGlnLySer 420
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QY      481 IleArgIleMetLySerHisValAlaLyArgLyPheLyGlyIuThrLeuArgProTyr 500
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QY      501 AspValLyAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
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DB      1666 AAAAGCTTCAAAACAGTGTATCAAAATCTTGAAAAAGGCAATTCACATCAGATAAG 1725
QY      541 LySerArgGlyLyIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
DB      1726 AAGAGCCGAGAAAATAACACAGAACATGAGACACAGAGATCTCATGTGCTCGGT 1785
QY      561 ArgValIleLyValGluLyGlnValGlnSerIleGlySerLyLeuAspCysLeuLeu 580
DB      1786 CGGTGTGTCAGAGTTGAAAAACAGGTACAGTCCATAGATCCAAAGCTGAGCCCTACA 1845
QY      581 AspIleTyrGlnGlnValLeuArgLyGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB      1846 GACATCTATCAACAGGTCTTGAAAAGGCTGCTGACCTCGCTTGTGCTTCATTC 1905
QY      601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLyS 620
DB      1906 CAGATCCACCTTTTGAATGTAACAGACATCTGACTATCAAAAGCCGTGTGATGCAAA 1965
QY      621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrAlaAsnIle 640
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Db 2026 TCGAGAGGCGCTGCAAGTTCAATTCGACGCCAAATGAGTTCACTGCCAGACTTTCTACGGG 2085
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QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
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Db 2086 CTTAGCCCTTAATGACAGTCAAGCAACACAGGTGCCAATTGATGAAGCGATGGCTCA 2145
| | | | |
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProAspProAlaAla 700
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Db 2146 GCAGTGGCAGCCCAACACACATTGGCAACCAATTAATACGACCCCAAGCCAGCAGCC 2205
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QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLeuHisLeuProArgProGlu 720
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QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
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Db 2266 ACTCTGACCCCTTAACCTCGAGGCTTAACAGAAAGCATTTCTGACCTCAACCTGCCCTT 2325
| | | | |
QY 741 ValAlaSerIleGlnValGlnValAlaGlnSerAsnLeuThrIleAspArgSerMet 760
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Db 2326 GTTGCTCCAGAGAAATGTTCAAGTTGCAAGTCAAAATCTCAACAGACCGTTCTATG 2385
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QY 761 ArgIleSerPheAspMetGlyGlyIleThrLeuLeuSerValCysProMetValProlys 780
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Db 2446 GACTTGGGCAAACTTTGTCTGTGCAAAACCTGATAGGTCAACCAAGAACCTGAATATA 2505
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QY 821 ArgGlnSerIleLeuPheIleThrAspGlnGluValGlyProGlnIleThrGlnThrAsp 840
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QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysIleAlaGlyIleSerThrAspAlaLeu 880
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RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3
Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 AspGlyLeuLeuLeuGlyThrArgAlaThrLeuGlyGlyGlyGlyLeu 40
| | | | |
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QY 41 ArgIleSerArgGlyIleGlnGlyAlaArgMetSerLeuGlyIleProLeuSer 60
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QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIleTyrArgGlyValGlnAsnTyrLeu 80
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QY 81 TyrAsnValLeuGlnArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
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QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIleLeu 120
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Db 585 ATCATTCGAATCTGCTGCGGGTTCGCTGTGATTAAGATAGGACAGGAAGACTG 644
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Db 885 GTTCTATATTTTGTCTTCTCTGTCTATCTGTGTGAGAAAGATGCAATPAAGATTT 944
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| | | | |

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DB 1005 GACAAACCTCCCTTAACCTGGCTGGAAAGATGCTTTCTGACAGCTTTCACCTTGGC 1064
QY 301 LLeSerPhePheAlaLeuProAlaGlyLLeuGlySerGlyPheAlaLeuLeuValGln 320
DB 1065 ATTTCTTTCTTTGACCTTCCGCGGCACTTCTGGCTCAGGTTTTCATTAAGTCAAA 1124
QY 321 GlnGlnHISArgGlnLysHISpHeGlnLysArgArgPheAlaAlaLeuLeuLLeGln 340
DB 1125 GAACAAACACCGCCGAAACCTTTGAGAAAGAAAGAACCCAGCTGCCAAGCTTATTCAG 1184
QY 341 CysValTrpArgSerTrpAlaAlaAspGlnLysSerValSerLLeAlaThrTrpLysPro 360
DB 1185 TGAGTTTGGGGTGGTGTACGACAGCTGATGAGAAATCTTTCCATTGCAACCTGGAAACCA 1244
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QY 441 LysProValLLeAspAlaAspThrAlaLeuGlyThrAspAspValTyraAspGlnLysGly 460
DB 1485 AAACCAAGTGAAGTGTGAACAGCCCTTGCACTATATGATATGATGATAAGAAAGGA 1544
QY 461 CysGlnCysAspValSerValGlnAspLeuThrProProLeuLysThrValLLeArgAla 480
DB 1545 TGCAGGTGATGATCAGTGAAGAGACTCACCCCACTTAAACATGTCATTCCAGACT 1604
QY 481 LLeArgLLeuLysPheHISValAlaLysArgLysPheLysGlnThrLeuArgProTyr 500
DB 1605 ATCAGATATTGAAATTTCAATGTTGCAGAAACGAAAGTTTAAAGAAACATTACCTCCATAT 1664
QY 501 AspValLysAspValLLeGlnGlnTyrSerAlaGlyHISLeuAspMetLeuCysArgLLe 520
DB 1665 GATGTAAAGATGTCATTGAAACAATATTTCTGCTGTCATCTGACATGTTGTAGAAATT 1724
QY 521 LysSerLeuGlnThrArgValAspGlnLLeuGlyLysGlnLLeThrSerAspLys 540
DB 1725 AAAAGCTTCAACACGCTGTTGATCAAAATCTTGGAAAGGCAAAATCAGATCAGATTAAG 1784
QY 541 LysSerArgGlnLysLLeThrAlaGlnHISGlnThrThrAspAspLeuSerMetLeuGly 560
DB 1785 AAAGAGCGAAGAAATTAACAGCAAGAACATGAGACCAAGATCTCAGTATGCTCGGT 1844
QY 561 ArgValValLysValGlnLysGlnValGlnSerLLeGlnSerLysLeuAspCysLeuLeu 580
DB 1845 CGGGTGTCAAGGTGAAAGAAACAGGTACAGTCCATTAACATCAAGCTGAGCTCTACTA 1904
QY 581 AspLLeTyrGlnGlnValLLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB 1905 GACATCTATCAACAGGCTCTTGGAAAGGCTCGCTCCACGCTCGTTGGCTTCAATTC 1964
QY 601 GlnLLeProProPheGlnCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB 1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGACATCAAGAGCCCTGTGATAGCAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrAlaAsnLLe 640
DB 2025 GATCTTTCCGGGTTCCGCAAAACAGGCTGCTTATCTCAGATCAACTATGCAACATC 2084
QY 641 SerArgGlnLysGlnPheLLeuThrProAsnGlnLysPheSerAlaGlnThrPheTyrAla 660

DB 2085 TCAGAGAGGCTGACGTTCAATTCGACGCCAAATGAGTCAAGTCCAGACTTTCTACGGG 2144
QY 661 LeuSerProThrMetHISerGlnAlaThrGlnValProLLeSerGlnSerAspGlySer 680
DB 2145 CTTAGCCCTTACTATGTGACAGTCAAGCAACACAGGTGCCAATTTGTCAAAGCGATGCTCA 2204
QY 681 AlValAlaAlaThrAsnThrLLeAlaAsnGlnLLeAsnThrAlaProLysProAlaAla 700
DB 2205 GCAGTGGACGCCCAACACCAATTCGAAACCAATTAATACGACACCCAGCCAGAGCC 2264
QY 701 ProThrThrLeuGlnLLeProProProLeuProAlaLLeLysHISLeuProArgProGly 720
DB 2265 CCAACAACCTTACAGATCCCACTCTCTCCAGCCATCAAGATCTGCCAGCCAGAA 2324
QY 721 ThrLeuHISProAsnProAlaGlyLeuGlnGlnSerLLeSerAspValThrThrCysLeu 740
DB 2325 ACTCTCACCCCTAACCTCGAGGCTTACAGAAAGATTTCTGACCTCACACCTGCTT 2384
QY 741 ValAlaSerLysGlnAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
DB 2385 GTTGCTCCAGGAAATGTTTCAGGTTGACAGTCAAAATCTCACAAAGACGCTTATAG 2444
QY 761 ArgLysSerPheAspMetGlyGlnThrLeuLeuSerValCysPrometValProLys 780
DB 2445 AGGAAAGGCTTTGACATGGAGAGGAAACCTGTTGTCTGTCTGTCATGCTGCCGAAG 2504
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuLLeArgSerThrGlnLLeuAsnLLe 800
DB 2505 GACTTGGGCAAAATCTTTGCTGTGCAGAAACCTGATCAGGTGCGCCAGAGAACTGAATATA 2564
QY 801 GlnLeuSerGlySerGlnSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
DB 2565 CAACTTTCAGGAGTGAAGTCAAGTGCCTCAGAGGCCAGCCAAATTTTAAACCAATGG 2624
QY 821 ArgGlnSerLysLeuPheLLeThrAspGlnGlnValGlyProGlnGlnThrGlnThrAsp 840
DB 2625 AGGGAATCCAAATTTGTTTAACTGATGAAGAGGTGGTCCGAAAGACAGAGACAGAC 2684
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArg 860
DB 2685 ACTTTTGATGCGCGACCGGAGCTTCGACAGGAAGCTGCTTGGCAACAATCTTCAAG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerLLeCysLysAlaGlyGlnSerThrAspAlaLeu 880
DB 2745 ACTGGAAGTCAAGATCAATCTCAGACATTTGTAAGGCGAGAAAGTCAAGATGCCCTC 2804
QY 881 SerLeuProHISValLysLeuLys 888
DB 2805 AGCTTGCTCCTCAGTCAAACTGAAA 2828

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kleke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Alignment Scores:

Pred. No.:	0	Length:	3111
Score:	4547.00	Matches:	888
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-810-796-5 (1-888) X US-10-803-268-3 (1-3111)

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QY      1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
DB      165 ATGAAAGGATGTGAGTCGGGCGGCGGAGGGTGGCTGTAACCTCGGACCGCGAGGGGC 224
QY      21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
DB      225 GACGGCTGCTACTGCTGGGACCCCGCGGCCACCTCGTGGCGGCGGCTGGCTTG 284
QY      41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB      285 AGGAGAGCGCGCGGCGGCAAGGAGGGGCGGATGAGCTGCTGGGAAAGCGGCTCT 344
QY      61 TyrThrSerSerGlnSerGlyArgArgAlaValTyrArgValGlnAlaTyrLeu 80
DB      345 TACACACAGTAGCCAGAGCTGCGCGGCAACGTCAATACCGCGGGTGCAGAACTACCTG 404
QY      81 TyrAsnValLeuGluLysProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB      405 TACACAGCTGCTGAGAGACCCCGCGGCTTATCTACACGCTTTCGTTTTTCTC 464
QY      101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIysLeu 120
DB      465 CTGTGCTTTGGTGTGATTTTGTTCAGTGTTTTTCACCATCCCTGAGCACAAATTG 524
QY      121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB      525 GCCTCAAGTTGCTCTTGATCTCTGGAGTTCTGATATGTCGTCTTTGGTGGAGTTC 584
QY      141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
DB      585 ATCATTGCAATCTGGTCTCGGCTTCTGTTCGATATAGAGATGCGCAAGAGACTG 644
QY      161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB      645 AGGTGTGCTCGAAAGCCCTTGTGTATAGATACCATGTCTTATCCCTCAATAGCA 704
QY      181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB      705 GTTGTTCGCAAAAACCTCAGGGTAATATTTTTCACGCTGCACTCGAAGTCTCCGT 764
QY      201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrPheLeuLeu 220
DB      765 TTCCTACACATCTCTCGCATGTGGCCACGACCGAAGGGAGGCACTTGGAAATTACG 824
QY      221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrIleGlyPheLeu 240
DB      825 GGTTTCAGTGGTTATCTCAGACAGCAAGAAATTATACAGCTTGGTACATAGGATTTTG 884
QY      241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB      885 GTTCTTAATTTTTCGCTTCTGTCTGTATCTGGTGAAGAGGCAATAAAGATT 944
QY      261 SerThrTyrAlaAspAlaLeuTyrPyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB      945 TCTACATATGACAGATCTCTCTGTGGGCAACAATTACATTGACACTATTGGCTATGGA 1004
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QY      281 AspLysThrProLeuThrTyrPheGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB      1005 GACAAAATCTCCCTTAATTGGCTGGAGATTTGCTTTCGACAGGCTTTCGACTCTTGGC 1064
QY      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB      1065 ATTCTTTCTTTGCACTTCCGCGGCAATCTTGGCTCAGGTTTGGCATTAAGATTACAA 1124
QY      321 GluGlnHisArgGlnLysHisPheGluLysArgArgAlaProAlaAlaAsnLeuIleGln 340
DB      1125 GACACACACCCCGCAGAAACACTTTGAGAAAAGAGAACCCAGCTCCCACTTCTTACG 1184
QY      341 CysValTyrPyrSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
DB      1185 TGTGTTTGGCGTATTTACGACAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1244
QY      361 HisLeuLysAlaLeuHisIleThrCysSerProThrArgGlnLysLeuSerPheLysGluArg 380
DB      1245 CACTTGAAGGCTTTCACACCTGACAGCCCTACCAATCAGAAAGCTTAAGTTTAAGAGCGA 1304
QY      381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
DB      1305 GTGCCCATGCTTAGCCCAAGGGGCCAGAGTATTAAGCCGACAAAGCTCAGTAGTGTAC 1364
QY      401 ArgArgSerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSer 420
DB      1365 AGGAGGTCCCAAGCAGCAGCATCACAGCCAGGCGCACTCCACCAAGTCAGAGAGAGC 1424
QY      421 TyrSerPheAsnAspArgThrArgPheArgProSerLeuArgLysLeuSerSerGlnPro 440
DB      1425 TGGAGCTTCACAGACCGAAACCGGCTTCGCGGCTTGCAGCTCCTCAAAAAGTTCTACGCCA 1484
QY      441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
DB      1485 AAACAGATGATAGTCGACACAGACCCCTTGCACTGATGATATAGTGAAGAAAAGGA 1544
QY      461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
DB      1545 TGCCAGTGTGATGATCAGTGAAGACCTCACCCACCACTTAAACCTGATTCGAGCTT 1604
QY      481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAspProLys 500
DB      1605 ATCAGAAATTATGAATTTTCATGTGCAACAGAAAGTTTAAGAAACATTACGTTCATAT 1664
QY      501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
DB      1665 GATGTAAGAATGTCATTTGAACATATTTCTGCTGTCATCTGACATGTTGTGTGAATTT 1724
QY      521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
DB      1725 AAAAGCCTTCAAAACCGTGTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAATAG 1784
QY      541 LysSerArgGluLysIleThrAlaGluHisGluThrTyrAspAspLeuSerMetLeuGly 560
DB      1785 AAGAGCCGAGAAATATACAGCAGACATAGACACAGATCTCAGATGTCTCGGT 1844
QY      561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
DB      1845 CGGGTGTCAAGGTTGAAAAACAGGTACGTCAATAGATCAAGAGCTGAGCTGACTTA 1904
QY      581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
DB      1905 GACATCTATCAACAGGTCTTTCGAAAGGCTCTGCTCAGCCCTTCGCTTGGCTTCATTC 1964
QY      601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB      1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATGCAAA 2024
QY      621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
DB      2025 GATCTTTGGGTTCCGCACAAAACAGTGGCTTATTCACATCAACTAGTGCACAACTTC 2084
QY      641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
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DB 2085 TCGAGAGGCTGAGTTCATTTGACGCCAAATGATTCAGTGCCGACCTTCTAGCGC 2144
QY 661 LeuSerProthmethisSerGlnalaThrglnvalProIleSerGlnSerAapGlySer 680
DB 2145 CTTAAGCCCTACTATGACAGCTCAAGCAACAGGTGCAATTAAGTCAAAAGCATGGCTCA 2204
QY 681 AlavalalaThraenthrilalaasnGlnIleasnThraIapProlyProalaala 700
DB 2205 GCAGTGGCACCCACCAACACATTGCAACCAATTAATACGGCACCCACCAAGCCAGCACC 2264
QY 701 ProthrThrlenglnIleProProProleuProalaIlelyshIleuProAargProglu 720
DB 2265 CCAACAACTTACAGATCCCACTCTCTCCAGACATCAAGCATGCGCCAGGCGAGAA 2324
QY 721 ThrlenuhIProenProalaIagIyleuGlnGlnSerIleSerAapValThrrThrybleu 740
DB 2325 ACTCTGACCCCTAACCTTGAGGCTTACAGAAAGCAATTTCTGACGTCACACCTGCTT 2384
QY 741 ValaIaserlyslubenValGlnvalaIaGlnSerAenleuthrlysaAparGserMet 760
DB 2385 GTTGCTCCAGAGAAATGTTCAAGTTGCAAGTCAATCTCAACAGACCGTTCTATG 2444
QY 761 ArglySerPheAapPheGlyglIurThrlleuSerValCysPProMetValProlys 780
DB 2445 AGGAAAAGCTTTGACATGGAGAGAAACTGTGTGTCTGTCTGTCCATGTGCGGAG 2504
QY 781 AapleuGlylyserSerleuSerValGlnaenleuIleAargSerThrgIugIuleuAenIle 800
DB 2505 GACTTGGGCAAACTTTGTCTGTGCAAAACCTGATCAGGTCGACGAGGAACCTGAATATA 2564
QY 801 GlnleuSerGlyserGlnSerSerGlySerAargGlySerGlnAapPheThrrProlySTTP 820
DB 2565 CAACCTTTCAGGAGTGAAGTGAAGTGGCTCCAGAGGACGCCAATTTTACCCCAATGG 2624
QY 821 ArgGlySerlysluPheIleThraPglIurGluValaGlyProgluIurThrgIurThraP 840
DB 2625 AGGGAATCCAAATGTTTATTAATCTGATGAAGAGTGGGTCCGAGAGACAGAGACAGAC 2684
QY 841 ThrrPheAapAlaIaIaProGlnProAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 860
DB 2685 ACTTTTATGATGCCACCGACGCTGCGAGGAAAGCTGCTTTCATCAGACTCTCAAG 2744
QY 861 ThrgIArgSerAargSerSerGlnSerIleCyleValaIaIaIaIaIaIaIaIaIaIa 880
DB 2745 ACTGGAAGCTCAGATCATCTTCAGACATTTTGAAGCAGAGAAAGTACAGATGCCCTC 2804
QY 881 SerleuProhIeValIysleuLys 888
DB 2805 AGCTGCCTCATGTCAAACTGAAA 2828
RESULT 6
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROUNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKHOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNG5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-866-020-1
Alignment Scores:
Pred. No.: 0
Score: 4527.50
Percent Similarity: 99.00%
Best Local Similarity: 98.89%
Query Match: 99.57%
DB: 9
Gaps: 1
US-09-810-796-5 (1-888) x US-09-866-020-1 (1-2694)
QY 1 MetLysAapValGlnSerGlyAargValIleuLeuAasnSerAlaIaIaIaIaIaIaIaIaIa 20
DB 1 ATGAAAGATGTGAGTCCGAGCCGAGGACAGGAGTCTTAATCTGGCAGCCGCGAGGAGC 60
QY 21 AapGlyLeuLeuLeuLeuGlyThraIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 40
DB 61 GACGGCTGCTACTGCTGGGACCCGCGGCAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 41 ArgGlySerAargGlylyslGlnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 60
DB 121 AGGGAAGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 61 TyrThrSerSerGlnSerCysAargAenValIysTyrAargValGlnAasnTyrIleu 80
DB 181 TACACAGATGACGACGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 81 TyrAasnValIeugIuAargProAargIlyTrpAlaPheIleThraIaIaIaIaIaIaIaIa 100
DB 241 TACAACGTGCTGAGAGAGACCCGCGGCTGGGCTTCATCAACAGCTTTCGTTTTC 300
QY 101 LeuValPheGlyCysleuIleuSerValPheSerThrrIleProGlnIleThrrlyslu 120
DB 301 CTGTGCTTGT 360
QY 121 AlaserSerCysleuLeuIleuGlnIleuPheValMetIleValaIaIaIaIaIaIaIaIa 140
DB 361 GCTTCAAGTGGCTCTTGAATCTGAGGATTCGATGATGATGATGATGATGATGATGATGATG 420
QY 141 IleIeIaargIleItrPserAlaGlyCysCysAargTyrAargIlyTrpGlnIaIaIaIa 160
DB 421 ATCATTCGAATCTGGATGCTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 161 ArgPheAlaIa 180
DB 481 AGCTTGTGCGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATCCCTTCAATAGCA 540
QY 181 ValIa 200
DB 541 GTTGTGTTCTGCAAAACCTCAGGAGTAAATTTTGGCAGCTCTGCACTCAAGATCTCCGT 600
QY 201 PheleuGlnIleleuAargMetValaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 220
DB 601 TTCCTACAGATCTCTCGATGAGTGGAGCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 221 GlySerValaIa 240
DB 661 GGTTCAGTGTATATGCTCAGCAGCAAGAAATTAACACAGCTTGTATACATAGAGATTTTGG 720
QY 241 ValIeuiIePheSerSerPheleuValIyrlleuValGlnIyAapAlaIaIaIaIaIaIa 260
DB 721 GTTCTTATTTTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
QY 261 SerThrTyrAlaAapAlaIa 280
DB 781 TCTACATATGACAGATGCTCTGTGTGGGCAAAATTAATGACAACTATTGGATAGGA 840
QY 281 AaplyThrProleuThrrIleuGlnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 300
DB 841 GACAAAACCTCCCTAACTTGTGAGGAAATTTGCTGTGACGAGCTTTCCTCTTGTGAC 900

Alignment Scores:

Prod. No.:	0	Length:	2694
Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.89%	Mismatches:	0
Query Match:	99.57%	Indels:	1
DB:	9	Gaps:	1

US-09-810-796-5 (1-888) x US-09-810-796-2 (1-2694)

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QY     21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db      61 GACGGCCTGTACTGCTGGGCAACCGCGCGCACTGTGTGGCGGGCGGTGGCTG 120

QY     41 ArgGluSerArgArgGlyGlnGlyValArgMetSerLeuLeuGlyLysProLeuSer 60
Db     121 AGGGAGAGCGCGCGGGCAAGCAGGGGGCCCGAGTGAAGCTCTGGGAAAGCGCTTCT 180

QY     61 TyrThrSerSerGlnSerCySarArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db     181 TACACGAGTAGCCAGAGCTGCGCGCGCAAGTCAAGTACCAGGGGGGTGCAGAACTACCTG 240

QY     81 TyrAsnValLeuGlyLysProArgGlyTyrAlaPheIleTyrThiAlaPheValPheLeu 100
Db     241 TACAACTGTGTGGAGAACCCCGCGGCTGGGCGTTCATCTACCAACGCTTTCGTTTCTC 300

QY    101 LeuValPheGlyCybLeuIleLeuSerValPheSerThrIleProGluIleThrLysLeu 120
Db     301 CTGTCTTGTGGTGTGATTTTGTCACTGTTTCTTCAATCCCTGAGCACAATAATG 360

QY    121 AlaSerSerCybLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db     361 GCGTCAAAGTGGCTCTTGATCTGGAGTTCGTGATGATTCGCTTGGTTGGAGTTTC 420

QY    141 IleIleArgIleTyrPserAlaGlyCybCybArgGlyTyrArgGlyTyrPglngIlyArgLeu 160
Db     421 ATCAATTCGAATCTGGTCTCGGGGTGCTGTTCGATATGAGAGATGGCAAGAAAGCTG 480

QY    161 ArgPheIleArgLysProPheCybValIleAspThrIleValLeuIleAlaSerIleAla 180
Db     481 AGGTTTGCTGAAAGCCCTTCTGTGTATAGATACCATGTGTTATCGCTTCAATAGCA 540

QY    181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db     541 GTTGTTCGCAAAAACCTCAGGGGTAATATTTTGGCCAGTCTGCACACAGATCTCCGT 600

QY    201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrLysLeuLeu 220
Db     601 TTCTCTCAGATCTCCGCGATGTGGCATGACCGAAGGGGAGGCACTTGGAATAATACCTG 660

QY    221 GlySerValValTyrAlaHiserLysGluLeuIleThrAlaTyrPyrIleGlyPheLeu 240
Db     661 GGTTTCAGTGTATATGCTTCAAGCAGAAATTAATTCACAGCTTGGTATCATAGAAATTTTG 720

QY    241 ValIleIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db     721 GTTCTTATTTTTTGTCTTTCCTTGTCTATCTGGTGAAGAAAGATGCAATAAAGGTTT 780

QY    261 SerThrTyrAlaAspAlaLeuTyrPglngIlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db     781 TCTACATATGCAATGCTCTCTGTGGTGGCACAATTACATTTGACATATTTGCTATGGA 840

QY    281 AspLysThrProLeuThrTyrPLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db     841 GACAAAACCTCCCTTACTTGGCTGGGAAGATTGCTTTCTCAGAGCTTTGCACTTCCTGGC 900

QY    301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db     |||
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Db     901 ATTTCTTTCTTTGACCTTCCTGCGGCACTTCTGTGCTCAGGTTTGTGATTAAGTACA 960
QY     321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db     961 GAACAACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCACACTCCCACTCATTCAG 1020

QY     341 CysValTyrPArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaThrTyrPLeuPro 360
Db     1021 TGTGTTGGGTATGTTATCCGACGCTGATGAGAAATCTGTTCCATTGCAACTGGAAAGCA 1080

QY     361 HisLeuIysAlaLeuHisThrCysSerProThr----- 371
Db     1081 CACTTGAAGGCTTGTGACACCTGACAGCTTCAACCAAGAAAGAACAGGGAGCATACGC 1140

QY     372 AsnGlnLysLeuSerPheLysGlyLysArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db     1141 AGTCAGAGCTTAAGTTTAAAGAGCAGTGGCATGGCTTACGCCAGGGGCCAGAGTATT 1200

QY     392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
Db     1201 AAGAGCCGACAGACCTCAGTATGTCACAGAGTCCCAAGACACGACATCACAGCCGAG 1260

QY     412 GlySerProThrLysValGlnLysSerTyrPserPheAsnAspArgThrArgPheArgPro 431
Db     1261 GGCAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAAGACGAAACCGCTTCCGGCCC 1320

QY     432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db     1321 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACACAGCCCTTGGC 1380

QY     452 ThrAspAspValTyrAspGlyLysGlnCysAspValSerValGluAspLeuThr 471
Db     1381 ACTGATGATATATATATATAAAGATGCCAGTGTGATATCAATGGAAGCTCACCC 1440

QY     472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db     1441 CCACCACTTAAAACTGCTACCTGACCTATCAGAAATATGAAATTTGATGTGGCAAAACCG 1500

QY     492 LysPheLysGluThrLeuArgProTyrAspValIleGluGlnTyrSerAla 511
Db     1501 AAGTTTAAGAAACGTTACGTCCATATGATGTAAGATGCTATTAACAAATTTGTGCT 1560

QY     512 GlyHisLeuAspMetLeuCybArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db     1561 GGTCACTGTGACATGTGTGTGTAATTAAGCTTCAAAACAGTGTGATCAAAATCTT 1620

QY     532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db     1621 GGAAAGGGCAAAATCAGTACAGTAAAGAGCCGAGAAATAACACAGAACATGAG 1680

QY     552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db     1681 ACCACAGACGATCTCGATGCTCGGGTGGGTGCTAAAGTTGAAAACAGGTACGTCCTC 1740

QY     572 IleGluSerLysLeuAspCybLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db     1741 ATTAGAGTCCAGAGTGAAGTCTGCTACTAGACATCTATCAACAGGTCTCTCGGAAGCTCT 1800

QY     592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGluGlnThrSer 611
Db     1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTGAAAGTGAACAGACATCT 1860

QY     612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCyb 631
Db     1861 GACTATCAAGCCCTGTGATGACAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC 1920

QY     632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db     1921 TTATCAAGATCAACTAGTCCAAACATCTCGAAGAGCTGTCAGATTCTTGAAGCCAAAT 1980

QY     652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db     1981 GAGTTCAGTCCAGACTTCTTACGCGCTTACGCCCTACTATGACACAGTCAAGCAACACAG 2040
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Qy	672	ValProIleSerGlnInserAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	691
Db	2041	GTGCCAATTAGTCAAAGCGATGGCTCAGACAGTGGACGCCACCAACCCATTGGCAAAACCA	2100
Qy	692	IleAsnThrAlaProLysProAlaAlaBroThrThrLeuGlnIleProProLeuPro	711
Db	2101	ATAAATACGCGACCCAAAGCCAGCAGGCCCCCAACAATTACAGATGCCACTCTCCCA	2160
Qy	712	AlaIleIysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGlu	731
Db	2161	GCCATTCAGACATCTGGCCAGGCCAGAAACTGTGACCTTAACCTTCAGAGGCTTACAGGAA	2220
Qy	732	SerIleSerAspValIleThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln	751
Db	2221	AGCATTTTCTGACGTCACACACTGGCTTGCTTCCCTCCAAAGAAATGTTCAAGTTGCACAG	2280
Qy	752	SerAsnLeuThrLysAspArgSerMetCArgLysSerPheAspMetGlyGluThrLeu	771
Db	2281	TCAAAATCTCACAAAGGACCGCTTCTATGAGAAAGCTTTGACATGGGAGGAAACTCTG	2340
Qy	772	LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu	791
Db	2341	TTTGCTGTCTGTCCCATAGTGTCCCAAGGACTTGGGCAAAATCTTGTCTGTGCAAAACCTG	2400
Qy	792	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg	811
Db	2401	ATCAGGTCGCACCGAGGAACGAAATATACAACTTTTCAAGGAGATGATCAAGAGGCTCCAGA	2460
Qy	812	GlySerGlnAspPheTyrrProLysThrArgLysSerLysLeuPheIleThrAspGluGlu	831
Db	2461	GGCAGCCAAAGATTTTTACCCCAAAATGGAGGGAAATCCAAATTGTTATTAACATGATGAAGAG	2520
Qy	832	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	851
Db	2521	GTGGGTCCCGAAGAGACAGACAGACACTTTTGATGGCCGACCGCAAGCCTGCCAGGGAA	2580
Qy	852	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	871
Db	2581	GCTGCCTTTGGATCAGACTCTCTAAGCACTGGAGAGTCACATCATCATCAGACGATTTGT	2640
Qy	872	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys	888
Db	2641	AAGCGACGAGAAATGACAGATGCCCTCAGCTTGCTCATGTCAAACTGGAA	2691
RESULT 8			
US-10-948-493-1			
; Sequence 1, Application US/10948493			
; Publication No. US20050064491A1			
; GENERAL INFORMATION:			
; APPLICANT: DMOBETEKY, STEVEN I			
; APPLICANT: RAMANATHAN, CHANDRA S			
; APPLICANT: TROUNACKI, JOANNE T			
; APPLICANT: BOISSARD, CHRISTOPHER G			
; APPLICANT: GRIBKOFF, VALENTIN K			
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: D0023 DIV			
; CURRENT APPLICATION NUMBER: US/10/948,493			
; CURRENT FILING DATE: 2004-09-23			
; PRIOR APPLICATION NUMBER: 60/207,389			
; PRIOR FILING DATE: 2000-05-26			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 2694			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-948-493-1			
Alignment Scores:			
Pred. NO.: 0			
Score: 4527.50			
Length: 2694			
Matches: 887			

Percent Similarity:		99.0%	Conservative:		1
Best Local Similarity:		98.8%	Mismatch:		0
Query Match:		99.5%	Indels:		9
DB:	21	Gaps:		1	
US-09-810-796-5 (1-888) x US-10-948-493-1 (1-2694)					
QY	1	MetLysASPValGluSerGlyArgGlyValLeuLeuAaNSerAlaAlaArgGly	20		
DB	1	ATGAAGAGTGTGAAGTCCGGCCGGGACGGGTCTGTCAACTCGCAGCCGCAAGGGC	60		
QY	21	ASPGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40		
DB	61	GAGGGCTCTACTGCTGGGGCACCCGGCCGGCCACGCTGTGGCGGGCGGTGGCTTG	120		
QY	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60		
DB	121	AGGGAAGCCCGCGGGACAGCAGGGGGCCGAGATGACCTTGCTGGGGACCCCTCTCT	180		
QY	61	TyrThrSerSerGlnSerCysArgArgAnValLysTyrArgArgValGlnAsnTyrLeu	80		
DB	181	TACACGATGACCAAGAGTCTCGGGGCAACGTCAAGTACCGCGGGGTGCAGAACTTACTG	240		
QY	81	TyrAsnValLeuGluArgProArgGlyTyrTrpAlaPheIleTyrHisAlaPheValPheLeu	100		
DB	241	TACAAAGTCTGTGAAGACCCCGCGGTGGCGGTTCATCAACAGCTTTCGTTTTCTC	300		
QY	101	LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu	120		
DB	301	CTTGCTTTGGTGGCTGATTTTGTCAAGTTTCTACACTCGCTGAGCACCAAAATTG	360		
QY	121	AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe	140		
DB	361	GCCTCAAGTGCCTCTTGATCTCTGAGATTCGTGATGATTCGCTTCCTTGGTTGGAGTTC	420		
QY	141	IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTyrTrpGlnLysArgLeu	160		
DB	421	ATCATTCGAATCTGGTCTCGGGGTTCGCTGTGTGCATTAAGAGATGGCAAGAAAGCTG	480		
QY	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180		
DB	481	AGGTTTGCTCGAAAGCCCTTGTGTATAGATVACATGTTCTTATCGCTTCAATGCA	540		
QY	181	ValValSerAlaLysThrGlnGlnLysIlePheAlaThrSerAlaLeuArgSerLeuArg	200		
DB	541	GTTGTTTCGCAAAACCTCAGGGTAAATTTTGGCACTGTGCATCAGAAAGCTCTCGT	600		
QY	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu	220		
DB	601	TTCCTACAAATCTCCGCAATGCTGGCATGAGCGAAGGAGGCACTTGGAAATTACTG	660		
QY	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240		
DB	661	GGTTCAGTGGTTTAAGCTCCACGCAAGGAATTAATCACAGCTTGTCATATGGAATTTTG	720		
QY	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260		
DB	721	GTTCTTAATTTTTCGTTCTTCTGTCTATCTGGTGGAAAGATGCCAATTAAGACTTT	780		
QY	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280		
DB	781	TCTACATATGCAAGATCTCTCGTGGGGCAAAATTACATTCAGAACATATGCTATGGA	840		
QY	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300		
DB	841	GACAAAAATCCCTTAATCTTGCGTGGAAAGATTGCTTTCGAGGCTTTCACCTCTTGGC	900		
QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320		
DB	901	ATTTCCTTTCTTGGCACTTCGCGGCAATCTTGCGCTCAGGTTTGGCATTTAAAGTCAA	960		
QY	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340		

Db 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCACACTCATTGAG 1020
Qy 341 CysValIITPrArgSerIYrAlaAlaAspGluYsSerValSerIleAlaThrTPrLyPro 360
Db 1021 TGTGTTGGGCGTGTATACGACAGCTGATGAGAAATCTGTTCCATTGCACACTGGAAGCA 1080
Qy 361 HaLeuYAlaLeuHISerThCySerProThr----- 371
Db 1081 CACTTGAAGGCTTGGCACACCTGCAGCCCTTACCAAGAAAGAACAGGGAGCATCAAGC 1140
Qy 372 AsnGluYsLeuSerPheYsGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAGAGTAAAGTTTAAAGAGCCAGTCCGATGGCTAGCCCGAGGGCCAGAGTATT 1200
Qy 392 YsSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAAACCCTCAGTAGGTGACGAGAGGTCCCAAGCACCAACATCACAGCCGAG 1260
Qy 412 GlySerProThrYsValGlnYsSerTPSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACAGCCGAAACCGCTTCCGAGCC 1320
Qy 432 SerLeuArgLeuYsSerSerGlnProYsProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTCGCCTCAAAAGTTCTCAGCCAAAACAGTGTAGATGCTGACACAGCCCTTGGC 1380
Qy 452 ThrAspAspValIYrArgGluYsGlyCyGlnCyAspValSerValGluAspLeuThr 471
Db 1381 ACTGAGAGATGATATATGATGAAAAAGATGCGACGTGATGATACAGTGGAGACCTCACCC 1440
Qy 472 ProProLeuYsThrValIleArgAlaIleArgIleMetYsPheHISValAlaYsArg 491
Db 1441 CCACCACTTAAACTGTCACTTCAAGCTATCAGAAATTTATGAATTTCACTGTGCAAAACG 1500
Qy 492 YsPheYsGluThrLeuArgProYrAspValIleGluGlnYrSerAla 511
Db 1501 AAGTTTAAGAAAGCTTACGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 512 GlyHISLeuAspMetLeuCyAspGlyIleYsSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCACTCTGGACATGTGTGTGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1620
Qy 532 GlyYsGluGlnIleThrSerAspYsYsSerArgGluYsIleThrAlaGlnHISGlu 551
Db 1621 GGAAGAGGCGAAATTCATCATCAGTATGAGAGAGCCGAGAGAAATTAACAGACAGACTGAG 1680
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValIleYsValGluYsGlnValGlnSer 571
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1740
Qy 572 IlegIleSerIleYsLeuAspCySLeuLeuAspIleYrGlnGlnValLeuArgYsGlySer 591
Db 1741 ATAGAGTCCAGAGCTGACCTGCTACAGCATATATCAACAGGTCTCTTGGAAAGGCTCT 1800
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluYsGlnGlnThrSer 611
Db 1801 GCCTCAGCCCTCGCTTGGCTTCACTTCATTCAGATCCCACTTTTAAAGTGAACAGACATCT 1860
Qy 612 AspTYrGlnSerProValAspSerIYsAspLeuSerGlySerAlaGlnAsnSerGlyCyS 631
Db 1861 GACTATCAAAAGCCTGTGATAGCAAAAGATCTTTCGGGTTCCGCAAAAACAGTGCCTGC 1920
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATTCAGATCAACTGTGCAACATCTCGAGAGGCTCGAGTTCATTTCAGAGCCCAAT 1980
Qy 652 GluPheSerAlaGlnThrPheTYrAlaLeuSerProThrMetHISerGlnAlaThrGln 671
Db 1981 GAGTTACGTGCCAGACTTTCTACGGCTTACGCCCTACATGACAGTCAAGCAACACAG 2040
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGAGTGGCAGCCCAACACCAATTGCAAAACCA 2100

Qy 692 IleAsnThrAlaProYsProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2101 ATAAATATGCGCACCCCAAGCCAGACAGCCCAACAACTTTACAGATCCACCTCTCCCA 2160
Qy 712 AlaIleYsHISLeuProArgProGluThrLeuHISProAspProAlaGlyLeuGlnGlu 731
Db 2161 GCCATCAACATCTGGCCAGGCCAGAAACTCTGCACCCCTAACCCCTCAGAGCTTACAGAA 2220
Qy 732 SerIleSerAspValIThrThCySLeuValAlaSerYsGluAsnValGlnValAlaGln 751
Db 2221 AGCATTTCTGACGTCAACCACTGCTTGTGCTTCCCAAGAAATTTTACAGGTTCACAG 2280
Qy 752 SerAsnLeuThrYsAspArgSerMetArgYsSerPheAspMetGlyGlyGluThrLeu 771
Db 2281 TCAAATCTCAACAGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAGAACTCTG 2340
Qy 772 LeuSerValCySProMetValProYsAspLeuGlyYsSerLeuSerValGlnAsnLeu 791
Db 2341 TTGTCTGTCTGTCCATGTGTCGGAAGAGACTTGGGCAATCTTGTCTGTGCAAAACCTG 2400
Qy 792 IleArgSerThGluGluLeuAsnIlegIleuSerGlySerGlySerGlySerArg 811
Db 2401 ATCAGGTCCAGCAGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGCCTCACA 2460
Qy 812 GlySerGlnAspPheTYrProYsTPArgGlySerIleYsPheIleThrAspGluGlu 831
Db 2461 GGCAGCCAAAGATTTTAAACCCCAATGAGAGGAATCCAAATGTTTAACTGATGAGAG 2520
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2521 GTGGGTCCGGAAGAGACAGACAGACACTTTTGTATGCCGACCGGACCTGCGAGGAA 2580
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCyS 871
Db 2581 GCTGCTTGCATCAGACTCTTAAGAGACTGGAAGGTCAAGATCACTCAGAGCATTTGT 2640
Qy 872 YsAlaGlyGluSerThrAspAlaLeuSerLeuProHISValIleYsLeuYs 888
Db 2641 AAGGACAGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAA 2691

RESULT 9
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 19 Gaps: 1

US-09-810-796-5 (1-888) x US-10-661-629-1 (1-3137)
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 QY 21 AAGGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 Db 61 GACGGCTGCTACTGCTGGGACACCGCGGCCACCTCGTGGCGGCGGCTGGCTTG 120
 QY 41 ArgGlySerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 121 AAGGAAAGCCGCGCGGGCAAGCAGGGGGCCGGATAGCCTGCTGGGAAACCGCTCTCT 180
 QY 61 TyrThrSerSerGlnSerCysArgArgAlaValTyrArgArgAlaGlnAsnTyrLeu 80
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 QY 81 TyrAsnValLeuGlyLysArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
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 QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
 Db 301 CTTCGCTTTGGTGTGATTTTGTCAAGTCTTTCTACCATCCCTGAGCAACAATAATTG 360
 QY 121 AlaSerSerCysLeuLeuIleLeuGlyPheValMetIleValValPheGlyLeuGlyPhe 140
 Db 361 GCCTCAAGTTGCTCTTGATCTCGAGTTCGATGATATTGTCGCTTTGGTGGAGTTC 420
 QY 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
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 QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleuLeuAlaSerIleAla 180
 Db 481 AAGTTTGCTCGAAAGCCCTTCTGTATATAGATACCATGTTCTTACCTTCAATAGCA 540
 QY 181 ValIleValSerAlaValThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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 Db 601 TTCCTACAGATCCTCGCATGCTGGCGCATGGAACGAAAGGGAGGCACTTGAATAATACG 660
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 Db 661 GGTTTCAGGTGATATCTCACAAGCAAGAAATTAATCACAGCTTGATACATAGATTGTTG 720
 QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAlaAsnLysGlyPhe 260
 Db 721 GTTCTTAATTTTTCGTCCTTCTTCTGTCATCTGGTGAAGAAAGGATCCCAATTAAGAGTTT 780
 QY 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyTyrHisIleThrLeuThrThrIleGlyTyrGly 280
 Db 781 TCTACATATGAGATGCTCTCTGCTGGGCAACAATTGACATTTGACATTTGGCTATGGA 840
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 Db 841 GACAAACCTCCCTTAACCTTGGCTGGGAAAGATGCTTTCGCAAGGCTTTCACCTCCCTGGC 900
 QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 Db 901 ATTTCTTTCTTTCGACTTCTCTGCGGCAATTCCTGGCTCAGGTTTTCATTTAAAGTACA 960
 QY 321 GlnGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
 Db 961 GAACAACACCGCCAGAAACCTTTGAGAAAGAAAGAACCCAGCTCCCAACCTCATTTGAG 1020
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 Db 1021 TGGTGTGGCGTAGTACGAGCTGATGAGAAATCGTTTCCATTCGCAACCTGGGAAGCCA 1080
 QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371

Db 1081 CACTGAAAGCCTTGACACCTGCAACCCCTTACCAAGAAAGAACAGGCAACATCAGC 1140
 QY 372 AsnGlnLysLeuSerPheLysGlyLysArgValArgMetAlaSerProArgGlyGlnSerIle 391
 Db 1141 AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGGCCAGGGGCCAGAGTATT 1200
 QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGly 411
 Db 1201 AAGACCCGACAAAGCCTCAGTAGGTGACAGAGGTCCCAAGACCGACATTCACACCGGAG 1260
 QY 412 GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro 431
 Db 1261 GGCAGTCCACCAAGCTGACAGAGAGCTTGAGCTTCAACGACCAACCCGCTTCGGGCC 1320
 QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
 Db 1321 TCGTGGCGGCTCAAAAGTTTTCAGCCAAACCAAGATATAGATGCTGACACACCGCTGGC 1380
 QY 452 ThrAspAspValTyrAspGlyLysGlyCysGlnCysAspValSerValGlyLysLeuThr 471
 Db 1381 ACTGATGATGATATATGAGAAAGAGATGCCAGTGTGATGATTCAGTGGAGAACCTCACCC 1440
 QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1441 CCACCACTTAANAACGTGATTCGAGCTATCAGAAATTAAGAAATTTCACTTCCAAACCG 1500
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 Db 1501 AAGTTTAAGAAACATTCAGTGCATATGATGATGATGATGATGATGATGATGATGATGATG 1560
 QY 512 GlnHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
 Db 1561 GGTCACTCGAGACATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGlnHisGly 551
 Db 1621 GGAAGAGGCGCAATATCACTCAGATAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
 QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGlyLysGlnValGlnSer 571
 Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGGGTCAAGAGTTGAAAGAACAGGTACAGTCC 1740
 QY 572 IleGlySerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
 Db 1741 ATAGAAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTCGGAAAGCTCT 1800
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlyCysGlnGlnThrSer 611
 Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCAACCTTTGGAATGGAACAGCATCT 1860
 QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 1861 GACTATCAAGGCCCTGTGGATGCAAAAGATCTTTCGGGTCCGCAAAACAGTGGCTGC 1920
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 Db 1921 TTATCCAGATCAACTAGTGCACAACATCTCGAAGAGCTGCACTATCTTGAGGCCAAAT 1980
 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 1981 GAGTTCAGTGGCCACACCTTTCAGCGGCTTAGCCCTTACTATGSCAAGTCAAGCAACAG 2040
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
 Db 2041 GTGCAATTTAGTCAAAAGGATGCTCCACAGTGGGAGGCAACCAACCACTTCCAAACCA 2100
 QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
 Db 2101 ATAAATAGGCAACCCAGGCAAGAGCCCAACCACTTACAAATCCACATCTCTCTCCCA 2160
 QY 712 AlaIleLysHisLeuProArgProGlyLysHisProAsnProAlaGlyLeuGlnGly 731
 Db 2161 GCCATCAAGCATCTGCCAGGCAAGCAAACTCTGACCCCTAACCTTCGAGGCTTACAGGAA 2220

QY 732 Ser1SerAspValThrThrCysLeuValAlaSerIysGluAsnValGlnValAlaGln 751
DB 2221 AGCATTTCTACGTCACCACTGCTGCTTGGCTCCAGAAATGTTCCAGGTTGCACAG 2280
QY 752 SerAsnLeuThrIysAspArgSerMetArgIysSerPheAspMetGlyGlyGlnThrLeu 771
DB 2281 TCAAATCTCACCAAGACCGCTTCTATGAGAAAAGCTTTGACATGGAGAGAAACTCTG 2340
QY 772 LeuSerValCysProMetValProIlyAspLeuGlyIlySerLeuSerValGlnAsnLeu 791
DB 2341 TTGTCTGTCTGCTCCATGCTGCGAAGACCTTGGCAATCTTGTCTGCAAAACCTG 2400
QY 792 ILAArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerIysSerGlySerArg 811
DB 2401 ATACAGTCGACCGACGACGAACTGAAATATACACTTTCAGGAGCTGATCAAGTCTCCAG 2460
QY 812 GlySerGlnAspPheTyrProIySTrPArgIlySerIlyLeuPheIleThrAspGluGlu 831
DB 2461 GGCAGCCAGATTTTAACTCCCAATGGAGGAAATCCAAATTTGTTTAACTGATGAAGAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
DB 2521 GTGGGTCGCCAAGACAGACAGACACACTTTGATGCTCCACCGCAGCTGCCAGGGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
DB 2581 GCTGCTTTCATCAGACTCTCTTAAGGACTGGAAGGTCAGACATCATCTCAGACATTTGT 2640
QY 872 LysAlaGlyCysSerThrAspAlaLeuSerLeuProHisValIlySerLeuIys 888
DB 2641 AAGGAGGAGAAAGTACAGATGCTCCTCAGCTTGCCTCATGTCAAACTGAAA 2691

RESULT 10
US-09-810-796-1
Sequence 1, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jergle, Timothy James
APPLICANT: ICGen, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1e1 Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3071
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-1
NAME/KEY: CDS
LOCATION: (10)..(2703)
OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

Alignment Scores:
Pred. No.: 0
Score: 4523.50
Percent Similarity: 98.89%
Best Local Similarity: 98.77%
Query Match: 99.48%
Length: 3071
Matches: 886
Conservative: 1
Mismatches: 1
Indels: 9
Gaps: 1
US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)

QY 1 MetLysAspValIleuSerGlyArgValIleuLeuAsnSerAlaAlaIleArgGly 20
DB 10 ATGAAGGATGTGAGTCGGGCGCGGGCAGGGTCTCTGAATCTGGCAGCGCCAGGGGCG 69

QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 70 GAGGCTCTGCTACTGCTGGGACCCGCGGCGCACCGCTTGAGCGCGGCTGGCTG 129
QY 41 ArgGluSerArgArgGlyIlyGlnGlyAlaArgMetSerLeuLeuGlyIlyProLeuSer 60
DB 130 AGGGAAGCGCGCGGGGACAGAGGGGGCCGGATGAGCTGCTGGGGAAGCGCTCTCT 189
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
DB 190 TACACAGTAGGACAGAGCTGCGCGCCCAACGTAACCTACCGGGGGTGCAGAACTCCG 249
QY 81 TyrAsnValLeuGluArgProArgIlyTTPAlaPheIleTyrHisAlaPheValPheLeu 100
DB 250 TACACGCTCTGAGAGACCCCGGCGGCTGAGGCTTCATCTACACGCTTCTGTTTCTTC 309
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrIlyLeu 120
DB 310 CTGTGCTTGGTTCGTGATTTTGTCAAGTCTTCTACCATCCTTGACACCAAAATTG 369
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValIlePheGlyLeuGluPhe 140
DB 370 GCTCAAGTTGGCTCTTGATCCTGAGTTCGATGATGTCGTCTTGTGTTGGAGTTC 429
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTTPGlnIlyArgLeu 160
DB 430 ATCATTCGATCTGCTCGGCTGCTGTGTGTCATGATGAGATGAGGACGAAACCTG 489
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 490 AGGTTTGCAGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATGCTTCAATAGCA 549
QY 181 ValValSerAlaIlyThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 550 GTTGTTCGCAAAACCTCAGGGTATATTTTGGCCACCTGCACTGCAAGTCCCGT 609
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyIlyThrTrpIlyLeuLeu 220
DB 610 TTCTTACAGATCCTCCGATGGTGGCATGACCGAAGGAGGACCTTGGAAATTACTG 669
QY 221 GlySerValIlyTyrAlaHisSerIysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 670 GGTTAGTGTTTATGCTCAGACAGAAAGATTAATCAGCTTGGTGAATGAGATTTTG 729
QY 241 ValLeuIlePheSerSerPheLeuValIlyLeuValGluLysAspAlaAsnIlyGluPhe 260
DB 730 GTTCTTATTTTTCGCTTCTTGTCTATCTGAGGAAAGATGCCAATAAGAGTTT 789
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 790 TCTACATATGACAGATGCTCTGTGGGACACAAATTAATGACAACTATGCTATGGA 849
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 850 GACAAACCTCCCTTAACCTTGGCTGGGAAGATTTCTTTCGACGCTTGCACTCTTGGC 909
QY 301 ILeserPhePheAlaLeuProIleGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 910 ATTTCTTCTTGGCACTTCTCCGCGCATTTGGCTCAGGTTTGGCATTAAGAATGACAA 969
QY 321 GlnGlnHisArgGlnIlyHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 970 GAACAACACCGCGAGAAACATTTGAGAAAGAAAGAACCCAGCTGCCAACTCATTCAG 1029
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1030 TGTGTTTGGCGTATGTTAGCACTGATGAGAAATCTGTTTCATTCGAACTGGAAGCCA 1089
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1090 CACTTGAAGCCCTTGACACCTGACAGCCCTTACCAAGAAAGAACAGGGAGCATCAAC 1149

QY 372 AaGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1150 AGTCAGAACCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCCAGAGTATT 1209
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1210 AAGAGCGCAGCAAGCCCTCAGTAGGTGACAGAGGTCCCAAGACCAACATCCAGCCGAG 1269
QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1270 GGCAGTCCCAACCAATGCGAAGAGCTGAGCTTCAAGACCGAACCCGCTCCGAGCC 1329
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1330 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACACAGCCCTTGGC 1389
QY 452 ThrAspAspValTyrArgGluLysGlyCyArgGlnCyAspValSerValGluAspLeuThr 471
Db 1390 ACTGATGATGATATATATGAAAAAGATGCGACGTGATGATCACTGGAAGACCTCAC 1449
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1450 CCACCACTTAAACTGTCAATTCAGACTATCAGAAATTATGAAATTTCACTTGGCAAAAC 1509
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1510 AAGTTTAAAGAAACCTTACGTCATGATGTAAAGATGTCTCATGAAACAAATTTCTGCT 1569
QY 512 GlyHisLeuAspMetLeuCyArgGlyLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1570 GGTCACTGTGACAGTGTGTGTAATTAAGCCTTCAAAACGTTGTATCAAAATTTCTT 1629
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGlnHisGlu 551
Db 1630 GGAAGAGGCAATCATCATCAGATTAAGAGAGCCGAGAGAAATTAACACAGACATGAG 1689
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1690 ACCACAGACGATCTCAGTATGCTCGGTGCTGCTGCAAGTTGAAAAACAGGTACAGTCC 1749
QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1750 ATGAAATCCAGAGTGAAGCTGCTCAGTACATTAACAAGGCTCTTGGAGAAAGCTCT 1809
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1810 GCTCAGCCCTGCTTGGCTTATTCAGATTCCTCCAGCTTTTGAAGTGAACAGATCT 1869
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1870 GACTATCAAAAGCCCTGTGATGCAAAAGATCTTTCCGGTTCGCGACAAAACAGTGTCTC 1929
QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1930 TTATCCAGATCACTAGTCCACATCTGAGAGGCTTGCAAGTCTTCTGAGCCCAAT 1989
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1990 GAGTTCAGTCCAGACCTTTCTACGCGCTTACGCCCTACTATGACAGTCAAGAACACAG 2049
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2050 GTGCCAAATTAAGTCAAAAGCATGTGCTCAGAGTGGCCACCAACCAATTTGCAAAACCA 2109
QY 692 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProLeuPro 711
Db 2110 ATAAATACGGACCCCAAGCAGACCCCAACCACTTACAGATCCCACTCTCTCCCA 2169
QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2170 GCCATCAAGCATGTGCCAGGCGCAAGAACTCTGCACCTTAACCTCAGGCTTACAGGAA 2229
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751

Db 2230 AGCATTTCTCAGCTCACCAACCTGCTGTGCTCTCAAGAAAAATGTCAGGTTGCACAG 2289
QY 752 SerLeuLeuThrLysAspArgSerMetArgLysSerPheAsnMetGlyGlyGlnThrLeu 771
Db 2290 TCAAAATCTCACCAAGACCGTGTATAGAGAAACCTTTGACATGGAGAGAAACTCTG 2349
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2350 TTGTCTGTCTGTCCATGATGTGCGAAGACCTTGGCAATCTTTGTCTGTGCAAAACCTG 2409
QY 792 IleArgSerThrGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2410 ATCAGCTGACCGAGAACTGATATACACTTTCAGGAGAGTCAAGTGCCTCCAGA 2469
QY 812 GlySerGlnAspPheTyrProLysTrpArgGlySerLysLeuPheIleThrAspGluGlu 831
Db 2470 GGCAGCCAAATTTTATCCCAATGAGAGGATCAAAATGTTTATATCTGATGAAGAG 2529
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
Db 2530 GTGGTCCCGAAGACAGACAGACACACTTTTATGTCGCGACCGCAGCTGCCAGGGA 2589
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2590 GCTGCTTTGATCATCACTCTCTTAAGACTGGAGGTCAAGTCACTTCACAGACATTTGT 2649
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2650 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAACTGAAA 2700

RESULT 11
US-09-813-148-1
; Sequence 1, Application US/09813148
; Parent No. US2002076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyValLeuAsnSerAlaAlaArgGly 20
Db 215 ATGAAGATGTGAGTCCGGCGGAGGGGTGCTGAACTCGGACGCCGCGAGGGGC 274
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40

Db	275	GACGGCCCTGCTACTCTGGGCAACCCGGCGGCACGCTTGTTGGCGCGCGGCGGCTGGCCCTG	334
QY	41	ArgGlnSerArgArgGlyYpGInglYAlAArgMetSerLeuLeuGlyYpSProLeuSer	60
Db	335	AGGAGAGAGCCGCGCGGGGCAAGACGGGGGCCCGGATGAGCTCTCTGGGAAGCCGCTCTCT	394
QY	61	TyrThrSerSerGlnSerCysArgArgaenValYpYrArgArgValGlnaenYrLeu	80
Db	395	TACACGAGTAGCCACAGAGCTGCCGGGCACACGTCAAGTACCGCGGGGTGCAGAACTACCTG	454
QY	81	TyrAenValLeuGlnaArgProArgGlyYrTrpAlaPheIleTyrHisAlaPheValPheLeu	100
Db	455	TACAAACGTGCTGGAGAGACCCCGCGCTGGGGCTTCATCTACACGCTTTCGTTTCCCTC	514
QY	101	LeuValPheGlyCysLeuLeileuSerValPheSerThrIleProGlnHisThrIlySLeu	120
Db	515	CTTGCTTTGGTGGCTGTGATTTTGTTCAGTGTTTCTTACATCCCTGAGACACAAATTGG	574
QY	121	AlaSerSerCysLeuLeuLeileuGlnPheValMetIleValValPheGlyLeuGlnPhe	140
Db	575	GCCCTCAAGTTGGCTCTTGATCCTGGAGTTCCGATGATGTGTCTGTTGTTGGAGTTCC	634
QY	141	IleIleIleArgIleTrrPseValaGlyCysCysCysArgGlyYrArgGlyYrTrpGlnYrArgLeu	160
Db	635	ATCATTTCAATCTGGTCTGGCGGGTGTGCTGTTTCGATATAGAGATGGCAGAAAGACTGC	694
QY	161	ArgPheAlaArgYpProPheCysValIleAapTrrIleValLeuIleAlaSerIleAla	180
Db	695	AGGTTTGCTCGAAACCCCTTCTGTGTATTAGATACCATTTGTTCTTATCCCTTCAATAGCA	754
QY	181	ValValSerAlaYpThrGlnGlyaenIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	755	GTTGTTTCTCGAAAAACTCAGGGTATATTTTGGCAGCTGCATCGACTGAGAGTCCGCT	814
QY	201	PheLeuGlnIleLeuArgMetValArgMetAapArgGlyGlyYrThrTrpIlySLeuLeu	220
Db	815	TTCCATCAGATCTCCCGCATGGTGGCATGGACCGAAGGGGAGGCACTTGGAAATTACG	874
QY	221	GlySerValValTyrAlaHisSerYpGlyLeuLeuIleThrAlaIleTrpYrIleGlyPheLeu	240
Db	875	GGTTACAGGTTTATGCTCACAGCAAGAAATTAACTACAGCTTGATCATAGAGATTTTGG	934
QY	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGlnYpAapAlaAenYpGlyPhe	260
Db	935	GTTCTTATTTTTCGTTCTTCTTGTCTATCTGGTGGAAAGATGCCAATTAAGATTT	994
QY	261	SerThrTyrAlaAapAlaLeuTrpTrpGlyYrThrIleThrLeuThrThrIleGlyYrGly	280
Db	995	TCTCATATGACAGATGCTCTCGTGGGGCACAATTACATTAACAATTTGGTATAGGA	105
QY	281	AapYpThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	1055	GACAAACCTCCCTTACTTGGCTGGAGAAATGCTTTCGACGAGCTTTGCACCTCTCTGGC	111
QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuYpValGln	320
Db	1115	ATTTCTTCTTTGCACTTCTCTGCGGCATTTCTTGGCTCAGGTTTGCATTAAAGTACA	117
QY	321	GlnGlnHisArgGlnYpHisPheGlnYpArgArgaenProAlaAlaHisLeuIleGln	340
Db	1175	GAAACAACCCGCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAATCTCATTTG	123
QY	341	CysValTrrPArgSerTyrAlaAlaAapGlnYpSerValSerIleAlaThrTrpIlyPro	360
Db	1235	TGTGTTTGGCTAGTTAGCACACTATGAAATCTGTTTCCATTGCAACTCGAAGCCA	129
QY	361	HisLeuYpAlaLeuHisThrCysSerProThr	371
Db	1295	CACTTGAAGGCTTGACACCTCGACCCCTACCAAGAAAGAACAGGGAGCATACAC	135
QY	372	AenGlnYpLeuSerPheYpGlnArgValArgMetAlaSerProArgGlyGlnSerIle	391

Db	1355	AGTCAAGAACTTAAGTTTAAAGAGCGAGTCCGATGGCTAGCCACCGGAGCCAGAGTATT	141
QY	.392	LYSSERARGINALASERVALGIYASPARGARSSERPROSERTHRASPILLETHRALAGLU	411
Db	1415	AAGAGCCGACAAGCCTCGTAGTGATGACAGAGAGTCCCGACAGACCGACATCACAGCCGAG	1474
QY	412	GLYSERPROTHLYRVALGINLYSSERTPSSERPLEAMNAPARGTHRARGPHEARGPRO	431
Db	1475	GGCAGTCCACCAAGGTCCAGAGAGCTGGAGGCTTCAACGACCGACCGGCTTCGGAGCC	1534
QY	432	SERLEUAQGLEUYSERSSERGLIPROLYSPROVALILEAPRALAASPTHRALAENGLY	451
Db	1535	TGCTGCCCTCCAAAAGTTCTCAGCCAAAACCGATGATAGTGGTGAACAGACGCTTTGGC	1599
QY	452	THRASPAEPVALTRYASPGLULYSGLYCYSGINCYASPAEPVALSERVALGIUASPLEUTHR	471
Db	1595	ACTGATGATGATATGATGATGAAAAAGGAGCCGACGTGTGATGATGATGATGAAAGACTCAC	1655
QY	472	PROPROLEULYSTRHVALILEARGALALEARGILLEWETLYSPHEHISVALALALYSARG	491
Db	1655	CCACCACTTAAAACTGCTCATTCGAGCTATCGAATTAGAAATTGAAATTTCAATGTTGCAAAACGG	1714
QY	492	LYSPHELYSGIUTHRLEUARGPROTHRASPVALLYSASPVALILEGLINTHYSERIAL	511
Db	1715	AAGTTTAAGAAACATTACGTCCATATGATATGAAAAAGTATGTCATTGAACAAATATTCCT	1774
QY	512	GLYHISLEUASPMELEUCYARGILEYSSERLEUGINTHRARGVALASPGNILELEU	531
Db	1775	GCTCATCTGCACATCTTGTGTGAAATTAAAAAGCTTCAACACGCTTGATCAAAATTCCT	1833
QY	532	GLIYLSGLYGINILETHSERASPLYLSYSERAGLIULYSILETHRALGLUHSGLU	551
Db	1835	GAAAAAGGCAAAATCACATCAGATPAGAGAGCCGAGAGAAAAATPACAGCAAGAACATGAG	1894
QY	552	THRTHRASPAPLEUSERMETLEUCIYARGVALYALLYSVALLGLULYSGINVALGLINSE	571
Db	1895	ACCACAGACGATCTCAGATGATCTCGGTGGGTGTCAGAGTTTGAAAAACAGATACAGTCC	1954
QY	572	ILEGLUSERLYSLEUASPYSLEULEUASPLILETRYGINGINVALILEUARGLYSGIYSE	591
Db	1955	ATGAGATCAAGAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGAAAAGGCTCT	2014
QY	592	ALASERALALEUALALEUALASERPHENILLEPROPROPHEGIUCYSGIUGINTHYSER	611
Db	2015	GCCTCAGCCCTCGGCTTGGCTTCAATCCAGATCCCACTTTTGAATGGAACAGACATCT	2074
QY	612	ASPTRYGINSESPROVALASPSERYLASPLEUSERGLYSERALAGINASERGLIYCS	631
Db	2075	GACTATCAAAACCCGTGTGATGAGCAAGATCTTTCGGGTTCGCGACAAACAGAGGCGTC	2134
QY	632	LEUSERARGSETRTHSERIALASNNILESERARGILEUGINPHEILEUETHPROASN	651
Db	2135	TTATTCAGATCAACTAGTGCACACATCTCGAGAGGCTTCGACGTTTCATTTCTACGCCAAT	2194
QY	652	GLUPHESERALAGINTHRPHERYALALEUSERPROTHMETHISSEGINALATHRGIN	671
Db	2195	GAGTTTACAGTGCACGACCTTCTAAGCGCTTACGCCCTACTAGACAGTCAAGCAACAACAG	2254
QY	672	VALPROILLESERGINSESPGLYSERIALVALALATHRASNTHRIEALASNGIN	691
Db	2255	GTGCCAAATTAGTCAAGAGGATGCTCAGCACTGGCAGCACCAACACCATTTGCAAAACCA	2314
QY	692	ILEANTHRALAPROLYSPROVALIAPROTHRTHREUGINILEPROPROPYLEUPRO	711
Db	2315	ATPAAATAGGAGCCCAAGCCAGACGCCCAACACTTACAGATCCCACTTCCTCTCCCA	2374
QY	712	ALALEYSHISLEUPROARGPROGLINTHREUHSIPROASNPROAGLYLEUGINGLU	731
Db	2375	GCATTCACAGCATCTGCCAGGCCAGAAACTGTGACCCCTAACCTCGACGCTTACAGGAA	2434
QY	732	SERILESERASPVALLTHRTHCYSELYVALALASERYSGIUAENVALGINVALAGIN	751
Db	2435	AGCATTTCTGACGTCACCACTGCGCTTGTGCTTCACAAAGAAAAATGTTACAGTTGCACAG	2494

QY 752 SerAsnLeuThrIysAspArgSerMetArgIysSerPheAspMetGlyGlyIuThrLeu 771
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Db 2495 TCBAATCTCAACCAAGACCGTTCTATGAGGAAAAGCTTTGACATGGAGGAGAACTCTG 2554
QY 772 LeuSerValCysPheMetValProIyAspLeuGlyIysSerLeuSerValGlnAsnLeu 791
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Db 2555 TTGTCTGTCTGTCTCCATGGTGGCCGAAGGACCTTGGGCAAAATCTTGTCTGTGGCAAACTCTG 2614
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
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Db 2615 ATAGAGTCCAGCCAGAACTGAATATACAACTTTCAGGAGATGAGTCMAAGTGGCTTCAAA 2674
QY 812 GlySerGlnAspPheTyrProIySTrPAArgIysSerIysLeuPheIleThrAspGluGlu 831
2675 GGCAGCCAGAGATTTTATACCCCAATGAGGGAATCCAAATTGTTATTAATGATGAAG 2734
QY 832 ValGlyProGluGluIuThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgIu 851
|||
Db 2735 GTGGGTCCCGAAGACAGAGACGACACTTTTGATGCGCACCGCAGCTCGCAGGAA 2794
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
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Db 2795 GCTGCTTTGTCATCAACTCTCTAAGGACTGGAAAGTCAAGATCACTCTCAGAGCAATTTGT 2854
QY 872 LysAlaGlyIysSerThrAspAlaLeuSerLeuProIleValIysLeuIys 888
2855 AAGGCAGAGAAAGTACAGATGCCCTCAGCTTCCATGTCMAACTGA 2905
Db

RESULT 12

US-10-482-834A-55
/ Sequence 55, Application US/10482834A
/ Publication No. US20050074764A1
/ GENERAL INFORMATION:
/ APPLICANT: Mulley, John Charles
/ APPLICANT: Harkin, Louise Anne
/ APPLICANT: Dibbens, Michelle
/ APPLICANT: Wallace, Robyn
/ APPLICANT: Phillips, Hillary Amy
/ APPLICANT: Heron, Sara Elizabeth
/ APPLICANT: Berkovic, Samuel Frank
/ APPLICANT: Scheffer, Ingrid Eileen
/ APPLICANT: Biomedics Limited
/ TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
/ FILE REFERENCE: 1386/17
/ CURRENT APPLICATION NUMBER: US/10/482,834A
/ CURRENT FILING DATE: 2004-01-02
/ NUMBER OF SEQ ID NOS: 173
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 55
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-482-834A-55

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
Db: 21 Gaps: 1

US-09-810-796-5 (1-888) x US-10-482-834A-55 (1-3074)

QY 1 MetLysAspValGlnSerGlyArgGlyValValIleLeuAsnSerAlaAlaArgGly 20
Db 215 ATGAAGGATGTGAGTCGGGCGGAGGAGTGTCTTAATCTGGCACCAGCGAGGGGC 274
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 275 GACGGCTCTGCTACTGTGGGCAACCGCGGCCACGCTTGTTGGCGCGCGGTGGCTTG 334

QY 41 ArgIysSerArgArgIlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
|||
Db 335 AGGAGAGAGCGCGGGGCAAGCAGAGGGGCCGAGTAGAGCTCTCTGGAAAGCCGCTCTCT 394
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
|||
Db 395 TACACGAGTAGCAGAGCTGCGGGCAACGTCAGATGCCGGGGGTGCAAGACTACCTG 454
QY 81 TyrAsnValIleuGlnAArgProArgIyTTrPaIlePheIleTyrAsnIleAlaPheValPheLeu 100
|||
Db 455 TACAACTGCTGAGAGAGACCCCGCGCTGGGCTTCACTACACAGCTTTCGTTTCCCTC 514
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluIleThrIysLeu 120
515 CTGTCTTGGTGGCTTGAATTTTGCAGTGTTTTACCATCTCGAGACCAAAATTGG 574
QY 121 AlasSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
|||
Db 575 GCTCAAGTGGCTCTTGAATCTCGAGATTCGATGATGTGTCTTGGTTGGAGTTC 634
QY 141 IleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
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Db 635 ATCATTCGAATGTGATCTGCGGTTGCTGTTCATATAGAGATGGCAAGAGACTG 694
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
695 AGGTTGCTCGAAACCCCTTCTGTGTATAGATACCATGTTCTTATGCTTCAATAGCA 754
QY 181 ValIleSerAlaIysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
|||
Db 755 GTTGTTCTGCAAAACTAGGGTATATTTTGCAGCTGCACTCGAAGTCTCCCT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgIyGlyThrTyrIysLeuLeu 220
|||
Db 815 TTCCTACAGATCTCGCATGTGTGGCAGATGACCGAAGGGAGGCACTTGAAATTAATG 874
QY 221 GlySerValValTyrAlaHisSerIysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
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Db 875 GGTTACAGTGTATAGCTCACAGCAAGAAATTAACACAGCTTGTATACATAGCAATTTTGG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
935 GTTCTTAATTTTTCGTTCTTCTGTCTATCTGTGAGAAAGATGCCAATTAAGATTT 994
QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
|||
Db 995 TCTACATATGAGAGATGCTCTGAGGGGCACAATTAATGACAACTATTGGCATGGA 1054
QY 281 AspLysThrProLeuThrTyrLeuGlyLysArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
1055 GACAAACCTCCCTTAACCTTGGCTGGAAAGATTGCTTTCGACGGCTTGCACCTTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
|||
Db 1115 ATTTCTTCTTTCGACTTCTGCGGCAATTCCTGACTAGGTTTGCATTAAAGTACAA 1174
QY 321 GlnGlnIleArgGlnLysIlePheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
|||
Db 1175 GAACAACAACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACTCATTCG 1234
QY 341 CysValIleTyrArgSerTyrAlaAlaAspGlyLysSerValSerIleAlaThrTyrLysPro 360
1235 TGTGTTTGGCGTATGTTAGCGAGCTGATAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuIleThrCysSerProThr----- 371
|||
Db 1295 CACTTGAAGGCTTTCACACCTGCGACCTTACCAAGAAAGAACAGGAGACATCAAC 1354
QY 372 AsnGlnLysLeuSerPheLysGlyLysArgValArgMetAlaSerProArgGlyGlnSerIle 391
|||
Db 1355 AGTCAGAAAGCTAAGTTTAAAGAGAGGAGTGGCATGGCTAGGCCCAAGGGGCAAGATATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

Db 1415 AAGAGCGAAGACCTCAGTAGGAGCAGAGGATCCCAAGCACCAGCATCACAGCGAG 1474
Qy 412 GlysSerProThrIy8ValGlnIySerTTPSerPheAaAapRgThraPheAaPro 431
Db 1475 GGGAGTCCCAACCAAGCAGAAAGAGCTGAGCTTCAACCAACCGAACCCGCTTCCGGCCC 1534
Qy 432 SetLeuAaRgLeuIySerSerGlnProIy8ProValIleAaPAlaAaPThraIleAaGly 451
Db 1535 TCGCTCGGCTCAAAAGTTCTCAGCCAAACAGTAGTAGTCTGACACAGCCCTTGGC 1594
Qy 452 ThrAaPArpValIyRgPglIyGlyCy8GlnCy8AaPArpIySerValGluAaPLeuThr 471
Db 1595 ACGTAGATGTATATGATGATAAAAGAGTGCAGTAGTATCATGAGGAAAGACCTCAC 1654
Qy 472 ProProLeuIy8ThrValIleAaGAlaIleAaGIlleAaIyPheAaIleValAaAaG 491
Db 1655 CCACCACTTAAACCTGTCATTCAGAGCTATCAGAAATTAAGAAATTTTCATGTTGCAAAACGG 1714
Qy 492 LysPheAaPLeuGlnThrLeuAaRgProIyRgAaPArpValIleGlnGlnIyR8SerAla 511
Db 1715 AAGTTAAAGAAACATTAAGCTCCATATGATGTATAAAGATGTCATTGAACAAATTTCTGCT 1774
Qy 512 GlnIleAaPArpLeuIyCy8AaRgIleIySerLeuGlnThraRgValAaPglIleIleu 531
Db 1775 GGTGATCTGGACATGTTGTGTAGAAATTAAGCCTTCAACCAAGTGTGATCAAAATTTCTT 1834
Qy 532 GlnIyGlyGlnIleThraSerAaPArpIy8LysSerAaRgIy8LysIleThraIleAaIy8Glu 551
Db 1835 GGGAAAGGGCAATCACTACATGATTAAGAAAGCCGAGAGAAATTAACAGAGAACTGAG 1894
Qy 552 ThrThraAaPLeuSerMetLeuGlyAaRgValIleValIy8LysGlnValIleGlnSer 571
Db 1895 ACCACAGACGATTCAGTATGCTCGGTGGGTGCTCAAGTTAATAAACAGGATACGCTCC 1954
Qy 572 IleGlnSerIy8LeuAaPArpIy8LysLeuAaPArpIleTyrGlnIleValIleuRgIy8Lys 591
Db 1955 ATGAGATCCAAAGCTGAGCTGCTTCTAGACATCTATCAACAGAGTCTCTGGAAAGGCTCT 2014
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCy8GlnIleThraSer 611
Db 2015 GCTTCAGCCCTCGCTTGGCTTCTTCAATCCAGATCCACCTTTGAATGTAACGACATCT 2074
Qy 612 AaPArpIy8LysSerProValAaPArpIy8LysLeuAaPArpIy8LysSerAlaGlnAaSerGlyCy8 631
Db 2075 GACTATCAAAAGCCTGTGATACCAAGATCTTCCGGTCCCAACAAACAGTGGCTGC 2134
Qy 632 LeuSerAaRgSerThraSerAlaAaPArpIy8LysLeuGlnPheIleuThraProAa 651
Db 2135 TTATCCAGATCAACCTAGTGCACATCTCGAGAGGCTGACAGTTCATTGACGCCAAAT 2194
Qy 652 GluPheSerAlaGlnThraPheIy8LysLeuSerProThraMetIleSerGlnIleAaThraGln 671
Db 2195 GAGTTACAGTCCCAAGCTTCTTACGGCTTACGCCCTTACATGACAGTCAAGCAACACAG 2254
Qy 672 ValProIleSerGlnSerAaPArpIy8LysSerAlaValAlaIleThraAaPArpIleAaGln 691
Db 2255 GTGCCAATTATGTCACCAAGCTGCTACAGCTGACGACCAACCAACCATTTGCCAAACCA 2314
Qy 692 IleAaPArpIleAaPArpIy8LysProAlaAaPArpThraLeuGlnIleProProIleuPro 711
Db 2315 ATAAATATACGCAACCAAGCAGACGCCCAACCAATTTACAGATCCACCTCTCCCA 2374
Qy 712 AlaIleIy8LysLeuProAaRgProGlnIleThraIleuIleProAaPArpAlaGlyLeuGlnIy 731
Db 2375 GCCATCAAGCATGTGCCAGGCAAGAACTGTACCTTAAACCTTCAGGCTTAAACAGGA 2434
Qy 732 SerIleSerAaPArpIy8LysLeuValAlaSerIy8LysAaPArpIy8LysValAlaGln 751
Db 2435 AGCATTTCTGACCTCACACCTGCTTGTGCTTCCAAAGAAATGTTCAAGTGTGACAG 2494
Qy 752 SerAaPArpIy8LysAaPArpIy8LysSerMetAaRgIy8LysSerPheAaPArpIy8LysIy8Lys 771

Db 2495 TCAAACTCACCAAGACCGTTCTATGAGAAAGCTTTGACATGAGAGAGAAACTCTG 2554
Qy 772 LeuSerValCy8ProMetValProIy8AaPLeuGlyIy8SerLeuSerValGlnIleu 791
Db 2555 TTGTCTGTGTCCTCCAGTGGTCCGAAAGACCTTGGGAAATCTTGTCTGTGCAAAACCTG 2614
Qy 792 IleAaRgSerThraGlnIleuAaPArpIleGlnLeuSerGlySerGlnSerGlySerAaRg 811
Db 2615 ATCAGGTGCAACGAGGAATGTAATATACACTTTTCAAGGAGAGTCAAGTGGCTCACA 2674
Qy 812 GlysSerGlnAaPArpIy8LysProIy8LysPArpIy8LysLeuPheIleThraPglIy 831
Db 2675 GCGAGCAAGATTTTATCCCAAAATGAGAGAAATCCAAATTTTATATCATATGAAGAG 2734
Qy 832 ValGlyProGlnIy8LysThraPArpThraPArpAlaIleProGlnProIleAaRgIy 851
Db 2735 GTGGGTCCGAAAGACCAAGACAGCACTTTTGAATCCGACCGAGCTCCAGGGAA 2794
Qy 852 AlaIleAaPArpIleSerAaPArpIy8LysThraRgIyAaRgSerAaRgIleSerIleCy8 871
Db 2795 GCTGCTTGTGATCAGACTCTTAAGAGACTGGAAGTCAAGTATCTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyIy8LysSerThraPArpIleuSerLeuProIleValIy8Lys 888
Db 2855 AAGCAGAGAGAAAGTAACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905

RESULT 13
US-10-399-489A-5
; Sequence 5, Application US/10399489A
; Publication No. US20050101004A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: ARGENTIERI, Thomas M.
; APPLICANT: SHELDON, Jeffrey H.
; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
; FILE REFERENCE: AM100620
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/241,078
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/32371
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/281,428
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-489A-5

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 21 Gaps: 1

US-09-810-796-5 (1-888) x US-10-399-489A-5 (1-3074)

Qy 1 MetLysAaPArpValGlnSerGlyAaRgIy8LysLeuAaPArpAlaIleAaRgIy 20
Db 215 ATGAAGATGTGAAGTCCGAGCCGAGGCAAGGTGCTGAACTCGACGCCCAAGGGGC 274
Qy 21 AaPglIyLeuIleuIleuGlyIy8LysAaPArpAlaIleAaPArpIy8LysIy8LysIy8Lys 40
Db 275 GACGGCTGTCTACTCTGAGGACCCCGCGGCGCAAGCTTGTGAGGGGGGGGGTGGCCG 334
Qy 41 AaRgIy8LysAaRgIy8LysGlnIy8LysAaRgMetSerLeuIy8LysIy8Lys 60
Db 335 AGGAGAGCCCGCGGGGCGCAAGGAGGGGCGGAGTGAAGCTGCTGCGAAAGCCGCTTCT 394

QY 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
Db 395 TACAGACGTAAGCCAGGCTGCCGCCCAACGTCAATACCGGGGGTGGAGAATCACTCG 454
QY 81 TyrAsnValLeuGlnArgProArgGlyTyrPalaPheIleTyrHisAlaPheValPheLeu 100
Db 455 TACAAAGTCTGAGAGAGACCCCGCGCTGGCTTCATCTACACACCTTCGTTTCCCTC 514
QY 101 LeuValPheGlyCysPheIleLeuSerValPheSerThrIleProGlnHisThrIlysLeu 120
Db 515 CTGTGCTTTGGTTCCTGATTTTGTACAGTCTTTTCAACATCCCTAGACACACAAATTG 574
QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLeuGlnPhe 140
Db 575 GCCTCAAGTTGCTCTTGAATCCTGAGATTCTGATGATGCTGCTTTGGTTGGAGTTTC 634
QY 141 IleIleArgGlyLeTyrSerAlaGlyCysCysArgTyrArgGlyTyrProGlnIleArgLeu 160
Db 635 ATCATTCGAATCTGCTCGGGGTTCTGTTCGTATAGATAGAGATGGCAAGGAAAGACTG 694
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 695 AGGTTTGCTCGAAAGCCCTTCTGTATATAGATACATTTGTTCTTATCCGCTTCAATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 755 GTTGTTCCTGCAAAACTCAGGGTAAATTTTGGCACGCTGCACTCAGAAAGTCTCGCT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrTrpIlyLeuLeu 220
Db 815 TTCTTACAGATCTCGCAGTGTGGCATGTGACGAGCGAAGGGAGGCACTTGGAAATTAACG 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240
Db 875 GGTTGAGTGGTTATCTCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGATTGTTG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlnLysAspAlaAsnLysGlnPhe 260
Db 935 GTTCTTAATTTTTTCGTTTCTTCTGTCTATCTGTGGAAAGGATCCAAATAAGAGTTT 994
QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyTyrIleThrLeuThrTrpIleGlyTyrGly 280
Db 995 TCTACATATGCAAGATCTCTGTGGTGGGACAAATTAATGCAACTATGTGGTATGGA 1054
QY 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCGACAGCTTGCATCTCTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1115 ATTTCTTTCTTGGCACTTCTCGCGGCAATTTCTTGGCTCAGGTTTTCATTAAAGTACAA 1174
QY 321 GlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaIleAsnLeuIleGln 340
Db 1175 GAACAACACCGCCGAGAAACCTTTGAGAAAGAGAGAACCCAGCTGCCAATCTTACG 1234
QY 341 CysValTyrPArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTrpLysPro 360
Db 1235 TGTGTTTGGCGTATGTAACGAGCTGATGAGAAATCTGTTTCCATTGCCAAGCTGGAGCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1295 CACTTGAAAGCCTTGACACCTGCAACCTTACCAGAAAGAACAGGGAGACATCAAGC 1354
QY 372 AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgIlyGlnSerIle 391
Db 1355 AGTCAAAGCTAAAGTTTAAAGAGCGAGTGGCATGGTCAAGCCGAGGAGCAAGATATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln 411
Db 1415 AAGAGCCGACAAAGCCTCAGTAAAGTGAAGAAGGTCCCAAGACCCGACATCAAGCCGAG 1474

QY 412 GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCAGTCCCAACCAAGTGCAGAAAGAGTTCGAGCTTCACAGACCAACCGCTTCCGGCCC 1534
QY 432 SerLeuAlaGlnLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1535 TCGTCGCGCTTCAAAAGTTCTCAGCCAAACCAAGATAGATGATGACACACGCTTGGCC 1594
QY 452 ThrAspAspValTyrAspGlnLysGlyCysArgLysCysAspValSerValGlnAspLeuThr 471
Db 1595 ACTGATGATGTATATGATGAAAGAAAGATCCAGTGTGATGTATCTAGTGGAGACTTCAC 1654
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1655 CCACCACTTAAACCTGATTCGAGCTATCAGAAATTATGAATTCATGTTCCAAACCGG 1714
QY 492 LysPheLysGlnThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAla 511
Db 1715 AAGTTTAAAGAAACATTACGTCCATATGATGTAAAGATGTCATTGAACTAATATTCTGCT 1774
QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1775 GGTCACTCGACATGTGTGTATGAATTTAAAGCTTCAACACGCTTGTATCAATTTCTT 1834
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGlnHisGln 551
Db 1835 GGAAGAAAGGCAAAATCATCATGATTAAGAGCCGAGAGAAATTAACAGCAGAAACATGAG 1894
QY 552 ThrThrAspAspLeuSerMetLeuGlnIleArgValLysValGlnLysGlnIleValGlnSer 571
Db 1895 ACCACAGACGATCTGATGCTCGGTGGGAGGTCAGAGTTGAAACAGGTTACAGTCC 1954
QY 572 IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATGAAATCCAAAGCTGAGCTGAGCTACTAGACATCTATCAACAGGCTCTCGAAGAGCTCT 2014
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATCCAGATCCCACTTTTGAATGTGAACAGACATCT 2074
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGCCCTGTGATATGCAAAAGATCTTGGGTTCCGACAAACAGTGCTGC 2134
QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTCGAGTTCAATCTGACGCCAAT 2194
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAGTGCACGACTTTCTACCGCGCTTAGCCCTTACTATGCAACAGTCMAAGCAACAG 2254
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAATGTCNAAGGATGGCTCAGCAGTGGAGGACCAACCAACATTTGCCAACAA 2314
QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2315 ATAAATACGGCACCCCAAGCCAGAGCCCAACCAACTTAAAGATCCACCTCTCTCCCA 2374
QY 712 AlaIleLysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGln 731
Db 2375 GCCATCAAGCACTGTGCCAGGCCAGAAACTGTGACCCCTTAACCTCGAGGCTTAAAGGAA 2434
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
Db 2435 AGCATTTCTGACGTACACACTGCTTGTGCTTCCAAAGAAATGTTCAAGTTGACACG 2494
QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLysThrLeu 771
Db 2495 TCAATATTCACCAAGAGACGTTCTATGAGAAAGCTTTGACATGAGAGAGAAACTCTG 2554
QY 772 LeuSerValCysPrometValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791

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Db 2555 TTGTCGTGTGTCCACGAGTGGCGAAGACTTGGGCAAACTTGTGTGTGCAAAACCTG 2614
Qy 792 TTAATGSerThrGluGluLeuAenILeGluLeuSerGlySerGluSerGlySerArg 811
Db 2615 ATAGAGTCGACCGAAGAACTGAATATACAACTTTCAGGGGAGTATGCAAGTGGCTCCAGA 2674
Qy 812 GATSerGlnAenPheThrProLysTPArgGluSerLysLeuPheIleThrAaPgluGlu 831
Db 2675 GCGAGCCAGATTTTATCCCAATGAGGGAATCCAAATTTGTTATTACTGATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAaPheThrPheAaPalaIleProGlnProAlaArgGlu 851
Db 2735 GTGGGTCGCCAAGACAGACAGACACTTTGATCCCGACCGAGCTGCCAGAGGA 2794
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Db 2795 GCTGCTTTGCACTCAACTCTCTTAAGACATGGAAGTCAAGATCATCTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyGluSerThrAaPalaLeuSerLeuProHlaValLysLeuLys 888
Db 2855 AAGCGAGAAAGTACAGATGCCCTCAGCTTCATGTCAAACTGAAA 2905

RESULT 14
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Scagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodriguez-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14195,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 11720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 64624, 84237, 8912, 2866,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MP102-018P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 55
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; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55
Alignment Scores:
Pred. No.: 9,846-198 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: 17 Gaps: 16

US-09-810-796-5 (1-888) x US-10-353-690-55 (1-2335)
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Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuAaArgGluSerArgArgLys 47
Db 166 ---CGTGCAGAGCAACAGGCGAGCGG-----CGGGGCGG 201
Qy 48 GInGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCGCCGCGCGCGCTCCGCTCCGCTCCGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCG 261
Qy 60 -----SerTyThrSerGlnSerCysAaArgAaAaValLysTy 73
Db 262 GCCGGCTCCGCGCTCCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 321
Qy 73 rATGArgValGlnAaenTyLeuTyAaAaValLeuGluAaArgProArgGlyTTPAlaPheI 93
Db 322 CCGCGCGCTCCGAGAACTGGGTCTTACACGCTGTGAAGCGCGCGCGCGCGCGCGCGCGCTT 381
Qy 93 eTyThAlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerTh 113
Db 382 CACACACGCTCATATTTTCTGCTGCTTACGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTG 441
Qy 113 rIleProGluHISrThLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetI 133
Db 442 TATCCAGGACGACCGAAGCTTGCACAAAGGTCTCCCTCATCTTGAATTCGTATGAT 501
Qy 133 eValValPheGlyLeuGluPheIleArgIleTTPSerAlaGlyCysCysAaArgTy 153
Db 502 CGGCTTTCCGCTTGAATCATGCTCCGGGTCTGCTGCGCGAGTGTGCTGCGCGG 561
Qy 153 rArgGlyTTPGInGlyArgLeuAaArgPheAlaArgLysPropheCysValIleAaPThrI 173
Db 562 CCGAGAGTGCAGAGGTCCGCTTCCGCTTCCGAGAAAGCCCTTCTGTCTATGACATTAT 621
Qy 173 eValLeuIleAlaSerIleAlaValAaSerAlaLysrThrGInGlyAaenIlePheAlaTh 193
Db 622 CGTGTTCGCGCTGCGCTGCGCTGCTCATCCCGGCTTACCCAGGGGCAACATCTTCCGCA 681
Qy 193 rSerAlaLeuAaSerLeuAaArgPheLeuGlnIleLeuAaMetValAaArgMetAaArgAr 213
Db 682 GTCCGCGCTCCGAGATGCGCTTCTGAGATCTTCCGCAAGTGTGCGCATGAGACCGCGG 741
Qy 213 gGlyGlyThrTTPLysLeuLeuGlySerValValTyAlaHisSerLysGluLeuIleTh 233
Db 742 CCGCGCGCACTGGAAGCTGCTGGGCTCAAGTGTCTTACCGGCAAGAGACTGATCAC 801
Qy 233 rAlaTTPTyIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyLeuValG 253
Db 802 CGCTGTGTACATCGGGTCTCTGTGTCTCATCTTCCCTTCCCTGCTTACCTGCGCCA 861
Qy 253 uLysAaPalaAaenLysGluPheSerThrTyAlaAlaPalaLeuTTPTPGlyTThrIleTh 273
Db 862 GAAAGACCAACTCGCACTTCTCTCTTACCGCACTGCTCTGTGTGGGAGCAATTAC 921
Qy 273 rLeuThrThrIleGlyTyArgLysPheLysThrProLeuThrTTPLeuGlyArgLeuLeu 293
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      982 TCGTGGCTTCGCTTACTGGGACATCTCTTTTGTGCTGCTGCGCGGACCTCTAGGCTC 1041
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      1042 CGGCTTGGCTGTGAAGACGAGACGACCGCGGAGAAAGCACTTCGAGAAACGCGAGAT 1101
Qy      333 nProAlaAlaSerLeuIleGlnIlyValIlyPheArgSerIlyrAlaAlaAsp---GlnIlySe 352
      1102 GCGGAGACCACTTATCATAGGCTGCTGCGCTGTACTCCACCGATATAGAGCGGAGC 1161
Qy      352 rValSerIleAlaThrTrp-----LysProHisIleuLeuAlaLeuHis 358
      1162 CTACCTGACAGCCACTGTGATCTACTATGACAGTATCTCCACTCTTCAGAGAGCTGGC 1221
Qy      358 ----- 358
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Qy      367 r-----CysSerProThrArgGlnIlyIleuSerPheIlyGlnArgVal 381
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Qy      381 lArgMetAlaSerProArgGlyGlnIleuSerIleuSerArgGln-----AlaSerValG 399
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Qy      399 yAspArgArgSerProSerIleuThrAlaIleuGlyIlySerProThrIlyValG 418
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Qy      418 nLysSerIlySerPheAsnAspArgThrArgPheArgProSerIleuArgLeuIlySerSe 438
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Qy      438 rGlnProIlyProValIleAspAlaAspThrAlaLeuGlyIlyThrAspAspValIlyrAspG 458
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Qy      478 eArgAlaIleArgIleMetIlySerPheHisValAlaIlySerGlySerPheIlyGlnIlyr 498
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Qy      538 rAspIlyIlySerArgGln-----LysIleThrAlaGlnHisGlnIlyThrThrAspAs 555
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      1918 AATCAGACATGATGGAGCGGTGTCAAGGTCAAGAGCAGGTGCATGATGAGACACA 1977
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RESULT 15
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTECH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127P052
; CURRENT APPLICATION NUMBER: US/10/850,928
; PRIOR APPLICATION NUMBER: 2004-05-20
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
; US-10-850-928-1

Alignment Scores:
Pred. No.: 9,84e-198 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: Gaps: 16

US-09-810-796-5 (1-888) x US-10-850-928-1 (1-2335)

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      166 ---CGTGCAGAGCCAAACAGGCGGAGCGGCG-----CGGGGCGCG 201

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 DB 262 GCCGCGCTCCGCGCTCGGCTCCGCTCGGCGCAAGCGCTCTCGGCGCGCAAGCGCTA 321
 QY 73 rArgArgValGlnAnTyThrLeuTyThrAnValLeuGlnArgProArgGlyTrrAlaPhe11 93
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 QY 113 r11eProGlnH1aThrLysLeuAlaSerSerCysLeuLeu11LeuGlnPheValMet11 133
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Search completed: October 23, 2005, 21:38:27
Job time : 1182 secs

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RESULT 2
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehe, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-3

Query Match 94.1%; Score 2890.8; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY 1 GGCAGCGGATGAAGATGTGAGTCCGGCCGGGGCAGGGTGTCTGTAAGCTCGGAGCC 60
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Db 156 GGCAGCGGATGAAGATGTGAGTCCGGCCGGGGCAGGGTGTCTGTAAGCTCGGAGCC 215
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QY 61 GCCAGGGGCGACGGCTCTACCTGAGGACCCCGCCGGCCACGCTTGGTGGCGGGC 120
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Qy 2101 GCAAAACCAATTAATACGAGCACAGAGCAGAGCCCAACCACTTATAGATGCCACCT 2160
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Qy 2221 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGTGCTTCAAGAAATGTTGAG 2280
Db 2349 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGTGCTTCAAGAAATGTTGAG 2408
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RESULT 3
US-09-813-148-1
/ Sequence 1, Application US/09813148
/ Patent No. 6617131
/ GENERAL INFORMATION:
/ APPLICANT: STEINMEYER, Klaus
/ APPLICANT: LERCHE, Christel
/ APPLICANT: SCHERER, Constanze
/ APPLICANT: SEEBOW, Guiscard
/ APPLICANT: BUSCH, Andreas E.
/ TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
/ FILE REFERENCE: 38005-119
/ CURRENT APPLICATION NUMBER: US/09/813,148
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: DE 100 13 732.6
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/194,041
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 93.0%; Score 2857.4; DB 4; Length 3074;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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 QY 2041 GCAACACAGAGTCCCAATTAAGTCAAGAGCTGCTGAGAGTGGGAGCCCAACCAATC 2100
 DB GCAACACAGAGTCCCAATTAAGTCAAGAGCTGCTGAGAGTGGGAGCCCAACCAATC 2246
 QY 2246 GCAACACAGAGTCCCAATTAAGTCAAGAGCTGCTGAGAGTGGGAGCCCAACCAATC 2305
 DB GCAACACAGAGTCCCAATTAAGTCAAGAGCTGCTGAGAGTGGGAGCCCAACCAATC 2305
 QY 2101 GCAAAACCAATTAAGTTCAGGCAACCAAGCAGAGCCCAACCAATTAAGTTCAGTCCACCT 2160
 DB GCAAAACCAATTAAGTTCAGGCAACCAAGCAGAGCCCAACCAATTAAGTTCAGTCCACCT 2160

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Db      2306 GCACCAATTAATATCGGACCCCAAGCCGACGCCCAACCTTTACAGATCCCACT 2365
Qy      2161 CCTCTCCCAAGCCATCAAGCATCTGCCAGGCGAGAACTCTGACCTTAACCTGACGGC 2220
Db      2366 CCTCTCCCAAGCCATCAAGCATCTGCCAGGCGAGAACTCTGACCTTAACCTGACGGC 2425
Qy      2221 TTACAGAAAAGCATTTCTGACGTCACCACTGCTGTTGTCCTCAAGAAAATGTTTCAG 2280
Db      2426 TTACAGAAAAGCATTTCTGACGTCACCACTGCTGTTGTCCTCAAGAAAATGTTTCAG 2485
Qy      2281 GTTGACAGTCAAAATCTCACAGAGACCTGTTATAGAGAAAAGCTTTGACATGGAGGA 2340
Db      2486 GTTGACAGTCAAAATCTCACAGAGACCTGTTATAGAGAAAAGCTTTGACATGGAGGA 2545
Qy      2341 GAAACCTGTGTCCTGTCCTGCCAGTGGTCCGAGAGAACTTTGGGCAAACTTTGTCTGTG 2400
Db      2546 GAAACCTGTGTCCTGTCCTGCCAGTGGTCCGAGAGAACTTTGGGCAAACTTTGTCTGTG 2605
Qy      2401 CAAACCTGATCAGTCCGACCGAGAACTGAATATACAACTTTCAGGAGTGAATCAAGT 2460
Db      2606 CAAACCTGATCAGTCCGACCGAGAACTGAATATACAACTTTCAGGAGTGAATCAAGT 2665
Qy      2461 GGCTCCAGAGGCGCCAAAGTTTTCACCCAAATGAGAGGAATCCAAATTTGTTTAACT 2520
Db      2666 GGCTCCAGAGGCGCCAAAGTTTTCACCCAAATGAGAGGAATCCAAATTTGTTTAACT 2725
Qy      2521 GATGAAGAGTGGTCCCGAAGAGACAGACACACTTTGATCCGACCGACGCT 2580
Db      2726 GATGAAGAGTGGTCCCGAAGAGACAGACACACTTTGATCCGACCGACGCT 2785
Qy      2581 GCCAGGAAAGCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGATCAAGATCATCTCAG 2640
Db      2786 GCCAGGAAAGCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGATCAAGATCATCTCAG 2845
Qy      2641 AGCATTTGTAAGCAGAGAGAAATACAGATGCTTCACTGCTTCAATCTGAAA 2700
Db      2846 AGCATTTGTAAGCAGAGAGAAATACAGATGCTTCACTGCTTCAATCTGAAA 2905
Qy      2701 TAAGTCTTCATTTCTTTCCAGGATAGAGTCTTTAGCCATACATATCATTTGATGA 2760
Db      2906 TAAGTCTTCATTTCTTTCCAGGATAGAGTCTTTAGCCATACATATCATTTGATGA 2965
Qy      2761 ACTATTTGAAAGCCCTTCTAATAAGTTGAATGCAAGATCGGAGAGAACTGAAG 2820
Db      2966 ACTATTTGAAAGCCCTTCTAATAAGTTGAATGCAAGATCGGAGAGAACTGAAG 3025
Qy      2821 CAGTTATAAGCCGTTACCTTTTAATGTCATGAAAATGATGTTTAG 2869
Db      3026 CAGTTATAAGCCGTTACCTTTTAATGTCATGAAAATGATGTTTAG 3074

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; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match      85.8%; Score 2635.4; DB 4; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy      1 GGACGGGATGAAGAGTGTGAGTCGGGCGGGGACAGGGTCTGTAACCTGGACGCC 60
Db      97 GGACGGGATGAAGAGTGTGAGTCGGGCGGGGACAGGGTCTGTAACCTGGACGCC 156
Qy      61 GCCAGGGGCGACGGCTGCTACTGCTGGGCAACCCGCGGCGACCGCTTGTGGCGGCG 120
Db      157 GCCAGGGGCGACGGCTGCTACTGCTGGGCAACCCGCGGCGACCGCTTGTGGCGGCG 216
Qy      121 GGTGCTTGAAGAGAGCCGCGGGGCAAGCAAGGGGCGCGGATGAGCCTGCTGGGGAAG 180
Db      217 GGTGCTTGAAGAGAGCCGCGGGGCAAGCAAGGGGCGCGGATGAGCCTGCTGGGGAAG 276
Qy      181 CCGCTCTCTTACAGAGTACGACAGCTGCGGCGGCAACGTCAATACCGCGGGTGCAG 240
Db      277 CCGCTCTCTTACAGAGTACGACAGCTGCGGCGGCAACGTCAATACCGCGGGTGCAG 336
Qy      241 AACTACTGTACCAAGTGTGAGAGACCCGCGGCTGGGCGCTTCACTACCAAGCTTTC 300
Db      337 AACTACTGTACCAAGTGTGAGAGACCCGCGGCTGGGCGCTTCACTACCAAGCTTTC 396
Qy      301 GTTTTCTCTCTGCTTTGTTGCTTGAATTTTGTCAAGTCTTCAATCCTTGACGAC 360
Db      397 GTTTTCTCTCTGCTTTGTTGCTTGAATTTTGTCAAGTCTTCAATCCTTGACGAC 456
Qy      361 ACAAAATTTGGCCCTCAAGTTGCTCTTGAATCTGAGATGCTGATGATGCTGTTGGT 420
Db      457 ACAAAATTTGGCCCTCAAGTTGCTCTTGAATCTGAGATGCTGATGATGCTGTTGGT 516
Qy      421 TTGAGTTCATCATTCGATCGATCGTCTGCGGTTCTGTTGCAATATAGAGATGCA 480
Db      517 TTGAGTTCATCATTCGATCGATCGTCTGCGGTTCTGTTGCAATATAGAGATGCA 576
Qy      481 GGAAGACTGAGGTTTGTGCGAAAGCCCTTCTGTGTTATAGATCAATGTTCTTATCGCT 540
Db      577 GGAAGACTGAGGTTTGTGCGAAAGCCCTTCTGTGTTATAGATCAATGTTCTTATCGCT 636
Qy      541 TCAATAGAGTGTTCGCAAAAACCTCAGGGTATATTTTTCACAGCTGCGACCTCAGA 600
Db      637 TCAATAGAGTGTTCGCAAAAACCTCAGGGTATATTTTTCACAGCTGCGACCTCAGA 696
Qy      601 AGTCTCCGTTTCTTACAGATCCTCCGATGCTGCGATGAGACCGAAGGGGAGCACTTGG 660
Db      697 AGTCTCCGTTTCTTACAGATCCTCCGATGCTGCGATGAGACCGAAGGGGAGCACTTGG 756
Qy      661 AAATTAAGTGGTTCAGTGGTTTATGCTCAACAGAAAGAAATTAATCAAGCTTGTATATA 720
Db      757 AAATTAAGTGGTTCAGTGGTTTATGCTCAACAGAAAGAAATTAATCAAGCTTGTATATA 816
Qy      721 GGAATTTTGTGTTCTTATTTTTCGCTTTCCTTGTCTTATCTGTTGGAAGAAAGATCCCAAT 780
Db      817 GGAATTTTGTGTTCTTATTTTTCGCTTTCCTTGTCTTATCTGTTGGAAGAAAGATCCCAAT 876
Qy      781 AAAGAGTTTTCATCATATGAGATGCTCTGTTGGGGGACAAATTAATCAATGCAACTAT 840
Db      877 AAAGAGTTTTCATCATATGAGATGCTCTGTTGGGGGACAAATTAATCAATGCAACTAT 936
Qy      841 GGCTATGAGACAAAACCTCCCTTAACCTTGGCTGGGAGATTGCTTTGACAGCTTTTGA 900
Db      937 GGCTATGAGACAAAACCTCCCTTAACCTTGGCTGGGAGATTGCTTTGACAGCTTTTGA 996
Qy      901 CTCCTTGGCATTTCTTTCTTTGCACTTCTGCGGGCATTTTGGGCTCAGGTTTTCATTA 960
Db      997 CTCCTTGGCATTTCTTTCTTTGCACTTCTGCGGGCATTTTGGGCTCAGGTTTTCATTA 1056

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RESULT 4
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0

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QY 961 AAAGTACAAAGAACACACCGCCAGAAAACCTTTGAGAAAAAGAGAACCCAGCTGCCAAC 1020
DB 1057 AAAGTACAAAGAACACACCGCCAGAAAACCTTTGAGAAAAAGAGAACCCAGCTGCCAAC 1116
QY 1021 CTCATTCAGTGTGTGTGGCGGTAGTTACGACAGCTGATGAGAAATCTGTTTTCATTTGCAACC 1080
DB 1117 CTCATTCAGTGTGTGTGGCGGTAGTTACGACAGCTGATGAGAAATCTGTTTTCATTTGCAACC 1176
QY 1081 TGGAAAGCCACATTTGAAAGGCTTGCACACTGCGACCCCTACCAAGAAAGAACAGGGGAA 1140
DB 1177 TGGAAAGCCACATTTGAAAGGCTTGCACACTGCGACCCCTACCAAGAAAGAACAGGGGAA 1220
QY 1141 GCATCAAGACAGTCAAGAGCTAAGTTTAAAGAGGAGTGGCAATGCTAGGCCAGGGGAG 1200
DB 1221 -----TCAGAAAGCTAAGTTTAAAGAGGAGTGGCAATGCTAGGCCAGGGGAG 1269
QY 1201 CAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGACAGAGAGTCCCAAGCAGCAGATC 1260
DB 1270 CAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGACAGAGAGTCCCAAGCAGCAGATC 1329
QY 1261 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGC 1320
DB 1330 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGC 1389
QY 1321 TTCGGGCGCTCGCTGCGCTCAAAAAGTTCTCAGCCAAACAGATGATAGTGCAGACAC 1380
DB 1390 TTCGGGCGCTCGCTGCGCTCAAAAAGTTCTCAGCCAAACAGATGATAGTGCAGACAC 1449
QY 1381 GCCCTTGACCTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATGAGTGA 1440
DB 1450 GCCCTTGACCTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATGAGTGA 1509
QY 1441 GACCTCACCCCACTTAAACCTGCTATTCGAGCTATCGAATTTATGAAATTTTCATGTT 1500
DB 1510 GACCTCACCCCACTTAAACCTGCTATTCGAGCTATCGAATTTATGAAATTTTCATGTT 1569
QY 1501 GCAAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGAAAAAGATGATGAAACAA 1560
DB 1570 GCAAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGAAAAAGATGATGAAACAA 1629
QY 1561 TATTCGTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1630 TATTCGTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689
QY 1621 CAAATTTCTGAAAAAGGCGAAATCATCATCATGATGAAAGAGCCGAGAGAAATTAACGCA 1680
DB 1690 CAAATTTCTGAAAAAGGCGAAATCATCATCATGATGAAAGAGCCGAGAGAAATTAACGCA 1749
QY 1681 GAACATGAGACACAGACGATCTCAGATGCTCGGTGCGGTGCAAGGTTGAAAAACAG 1740
DB 1750 GAACATGAGACACAGACGATCTCAGATGCTCGGTGCGGTGCAAGGTTGAAAAACAG 1809
QY 1741 GTACAGTCCATAGATTCAGAGCTGAGCTGCTTCTAGACATCTTATCAACAGTCTCTCG 1800
DB 1810 GTACAGTCCATAGATTCAGAGCTGAGCTGCTTCTAGACATCTTATCAACAGTCTCTCG 1869
QY 1801 AAAGGCTCTGCTCAGAGCCCTGCTTGGCTTTCATTCAGTTCCCACTTTTGAATGAA 1860
DB 1870 AAAGGCTCTGCTCAGAGCCCTGCTTGGCTTTCATTCAGTTCCCACTTTTGAATGAA 1929
QY 1861 CAGACATCTGATCATCAAAAGCCCTGAGATGAGAAAGATTTTGGGTTCCGACAAAAC 1920
DB 1930 CAGACATCTGATCATCAAAAGCCCTGAGATGAGAAAGATTTTGGGTTCCGACAAAAC 1989
QY 1921 AGTGGCTGCTTATTCAGATCAACTAGTGCAGACATCTCGAGAGCCCTGACGTTCAATTCG 1980
DB 1990 AGTGGCTGCTTATTCAGATCAACTAGTGCAGACATCTCGAGAGCCCTGACGTTCAATTCG 2049
QY 1981 AGCCCAAAATGATTCAGTGGCCAGACTTTTACGCGCTTAGCCCTACTATGACAGTCAA 2040
DB 2050 AGCCCAAAATGATTCAGTGGCCAGACTTTTACGCGCTTAGCCCTACTATGACAGTCAA 2109

QY 2041 GCAACACAGGTGCAATTAAGTCAAGAGATGCTCAGACGTGGCAGCCACCAACCATTT 2100
DB 2110 GCAACACAGGTGCAATTAAGTCAAGAGATGCTCAGACGTGGCAGCCACCAACCATTT 2169
QY 2101 GCAAAACCAATTAATACGGGACCCCAAGCAGCAGCCCAACCACTTTACAGATCCACCT 2160
DB 2170 GCAAAACCAATTAATACGGGACCCCAAGCAGCAGCCCAACCACTTTACAGATCCACCT 2229
QY 2161 CCTCTCCAGCCATCAAGATCTGCCAGGCCGAAACTCTGACCTTAACCTTCAGAGC 2220
DB 2230 CCTCTCCAGCCATCAAGATCTGCCAGGCCGAAACTCTGACCTTAACCTTCAGAGC 2289
QY 2221 TTACAGAAAGCAATTTCTGACGTCACCACTGCTGTTGCTCCCAAGGAAAAATGTTCCAG 2280
DB 2290 TTACAGAAAGCAATTTCTGACGTCACCACTGCTGTTGCTCCCAAGGAAAAATGTTCCAG 2349
QY 2281 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2340
DB 2350 GTTGCAAGTCAATCTCAACCAAGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGA 2409
QY 2341 GAAACTCTGTCTGTCTGTCTGCCATGCTGCCGAAAGACTTTGGGCAATCTTTGTCTGTG 2400
DB 2410 GAAACTCTGTCTGTCTGTCTGCCATGCTGCCGAAAGACTTTGGGCAATCTTTGTCTGTG 2469
QY 2401 CAAAACTGATCAGTGCAGCCGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGT 2460
DB 2470 CAAAACTGATCAGTGCAGCCGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGT 2529
QY 2461 GGTCTCAGAGGACCCCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTATTAAT 2520
DB 2530 GGTCTCAGAGGACCCCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTATTAAT 2589
QY 2521 GATGAAGAGTGGGTCCCAAGAGACAGACAGACACTTTTGATGATGCCGACCGGACCT 2580
DB 2590 GATGAAGAGTGGGTCCCAAGAGACAGACAGACACTTTTGATGATGCCGACCGGACCT 2649
QY 2581 GCCAGGGAAGCTGCTTTCATCAGACTCTTAAGAGCTGAAAGTCAAGATCATCTCAG 2640
DB 2650 GCCAGGGAAGCTGCTTTCATCAGACTCTTAAGAGCTGAAAGTCAAGATCATCTCAG 2709
QY 2641 AGCATTTGTAAGGACAGAGAAAGTACAGATGCCCTCAGCTTCATGATCAAACTGAAA 2700
DB 2710 AGCATTTGTAAGGACAGAGAAAGTACAGATGCCCTCAGCTTCATGATCAAACTGAAA 2769
QY 2701 TAA 2703
DB 2770 TAA 2772

RESULT 5
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823

Query Match 16.9%; Score 518; DB 4; Length 2196;
 Best Local Similarity 60.1%; Pred. No. 5e-145;
 Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

QY 226 TACCGCGGGGTGACAACTACCTGTACAAAGTGTGGAAGAGACCCGCGGCTGGGGCTTC 285
 DB 181 TACCGCGGGGTGACAACTACCTGTACAAAGTGTGGAAGAGACCCGCGGCTGGGGCTTC 240
 QY 286 ATCTACACGACCTTCTGTTTCTCTGTGTTGTTGCTGATTTTGTCAAGTATTTCT 345
 DB 241 GTCTACACGACCTTCTGTTTCTCTGTGTTGTTGCTGATTTTGTCAAGTATTTCT 300
 QY 346 ACCATCCCTGAGACACAAAAATGAGCTCAAGTTCCTTGAATCTGAGATTCGTATG 405
 DB 301 ACTATCCAGAGACACAGAGAACTTGCACAAAGATGCTCTCATCTTGAATTCGTATG 360
 QY 406 ATTTGCTCTTTGGTTTGGATTCATCATTCGAAATCTGCTGCGGGTGTCTGTTGCA 465
 DB 361 ATCTGCTTTTGGCTTGGATTCATCATTCGCGGGTGTCTGCTGCGGGTGTCTGCTGCGC 420
 QY 466 TATAGAGATGACGAAGAAGTGAAGTTCGCAAGAGCCCTTCTGTATATGATAC 525
 DB 421 TACCGAGATGAGAGAGGTGCTTCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 480
 QY 526 ATTTGCTTATGCTTCAATAGCAGTGTGTTTTCGAAAACTCAGGGTATATTTTTC 585
 DB 481 ATCTGCTTATGCTTCAATAGCAGTGTGTTTTCGAAAACTCAGGGTATATTTTTC 540
 QY 586 AGCTGTCATCAGAGATCTCCGTTTCTCAAGATCTCCGATGTTGGGATGAGACCA 645
 DB 541 AGCTGTCATCAGAGATCTCCGTTTCTCAAGATCTCCGATGTTGGGATGAGACCA 600
 QY 646 AGGAGAGACCTTGAATAATTAAGTGTGATGTTTATGCTCAAGAGAAATTAATC 705
 DB 601 CGCGGGGACCTGGAAGCTGCTGGGCTCAGTGTCTAGCGGATAGCAAGAGAGCTGATC 660
 QY 706 ACAGCTTGTATCAGATTTTGTGTTCTTATTTTTCCTTCTGTTCTATCTGATG 765
 DB 661 ACCGCTGTGATCATCGGGTTCCTGTCATCTTGCTCTCTGCTTCACTGAGCT 720
 QY 766 GAAAGAGATGCAATAAGATTTTCTACATAGCAGATGCTCTGAGGGGCAAT 825
 DB 721 GAAAGAGATGCAATAAGATTTTCTCTCTCTAGCGGATGCTGCTGAGGGGCAAT 780
 QY 826 ACATAGCACTATGCTATGAGACAAATCTCCCTAATCTGCTGGAGAAATGCTT 885
 DB 781 ACATAGCACTATGCTATGAGACAAATCTCCCTAATCTGCTGGAGAAATGCTT 840
 QY 886 TCTGACGCTTGGCACTCTTGGCAATTTCTTTTTCACCTTCGCGCATTTCTG 945
 DB 841 GCTGCTGGCTTGGCACTCTTGGCAATTTCTTTTTCACCTTCGCGCATTTCTG 900
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 QY 1066 GTTTCATTTGCACTTGAAGCCACCTTGAAGGCTTGAACCTGCACTGCACTG 1116
 DB 1021 GCTTACCTACAGCCACTGTGATCTATGACAGATCTCTCCATCTTTCAGAGAGCTG 1080
 QY 1117 CCTACCAAGAAAGAAAGAGAGAGATCAAGCAGTCAAGAGTA----- 1161
 DB 1081 GCTCTCTTTGTTGAGACGTGCAAGGAGCCGCAATGAGGAGCTTACGAGGCTG 1140
 QY 1162 ----- 1161
 DB 1141 CGGCGGGGCGCGGTACCGAGAGACACCTCCGTTACCCGCGCTTGGCACTGCGCAC 1200

QY 1162 -----AGTTTAAAGAGCGA 1176
 DB 1201 CGGCGGGAGACACTCTCTTGTGCGCTGGGAAAGACCGGATGGGATCAAAAGACGC 1260
 QY 1177 GTGGCAGTGGCTAGGCCCGAGGGCCAGA-----CTATTAGAGCGCAAGCCCTCAGTA 1230
 DB 1261 ATCCGATGAGGAGCTCCAGGCGGAGCGGATCTTCCAGAGACATCTGCACTTCCA 1320
 QY 1231 GGTGACAGAGGTTCCTCCAGAGACCGCATCAAGCCGAGG--GCAGTCCCAAGAGTG 1287
 DB 1321 ACAATGCCCACTCCCAAGAGAGGAGAGGATGGGTGAGGCGACAGCCGACCAAGGTG 1380
 QY 1288 CAGAAAGCTGAGAGCTTCAAGACCGAACCCGCTTCGCGCCCTGCTGCGCTCAAAAGT 1347
 DB 1381 CAAAAGACTGAGAGCTTCAATGACCGACCCGCTTCGAGGACATCTCTAGACTC----- 1434
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 QY 1468 ATTGAGCTATCAGATTTATGAAATTTTATGTTGCAAAAAGAGATTTAAGAACTTTA 1527
 DB 1543 ATCCCTCATCAGATTTCTCAAGTTCTGTTGCGCAAAAGAAATTTCAAGAGACACTG 1602
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 DB 1603 CGACCTTACAGCTGAAAGAGCTCTTATGACAGTACTAGCAGGCGCACTGACATGCTG 1662
 QY 1588 TGTGAATTTAAAGCCCTTCAACAGTGTGATCAAAATTTTGGAAAAAGGC--AAATC 1644
 DB 1663 GCGCGGATCAAGAGCTGCAAACTCGGATGAGCAAAATTTGTGAGTGGGGGCCGAGAC 1722
 QY 1645 ACATGAGATTAAGAAAGCGGAGAGAAATTAACAGAGAAATGAAACACAGACATCTC 1704
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 QY 1705 AGTATGCTCGGTGCGGTGATCAAGGTTGAAAAAACAGTATGATGATGATGATGATGAT 1764
 DB 1783 AGCATGATGAGACGCTGTGTGATGAGTGAAGAGAGTGTGATGATGATGATGATGAT 1842
 QY 1765 GACTGCTACTAGACATCTATCAAGGTCTTTCGAAAAGCTTGTGCTCAGCCCTGCT 1824
 DB 1843 GACTGCTGTGAGGCTTCTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1896
 QY 1825 TTGCTTATTTCCATTTCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1884
 DB 1897 CTGGGCGCGTGAAGTCCGCTGTTGACCCCGACATCACTCCGACTACCAAGCCCT 1956
 QY 1885 GTGATAGCAAAAGATCTTTCGGGTTCCGACAAA 1918
 DB 1957 GTGACACAGAGACATCTCCGCTCTCCGACAGA 1990

RESULT 6
 US-09-492-361-1
 ; Sequence 1, Application US/09492361
 ; Patent No. 6794161
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTISCH, Thomas J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
 ; TITLE OF INVENTION: POTASSIUM CHANNELS
 ; FILE REFERENCE: 2815-127P
 ; CURRENT APPLICATION NUMBER: US/09/492,361
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2335
 ; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 16.9%; Score 518; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 5.3e-145;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

226 TACCGCGGCGGAGAGAACTACCTGACAGCTGAGAGAGACCCCGGCTGGGCTTC 285
Db TACCGCGGCTGGAGAACTGGGTCTACAGTGTGTGAGGGGCCCGGCTGGGCTTC 379
320 TACCGCGGCTGGAGAACTGGGTCTACAGTGTGTGAGGGGCCCGGCTGGGCTTC 379
QY 286 ATCTACGAGCTTTCGTTTTCCTCTGCTTGTGCTTGAATTTTGTCAAGTTCCT 345
Db GTCTACGAGCTTTCGTTTTCCTCTGCTTGTGCTTGAATTTTGTCAAGTTCCT 439
QY 346 ACCATCCCTGAGACACAAATTTGGGCTCAAGTTGGCTTGAATCCCTGAGTTCGTATG 405
Db ACTATCCAGAGACACAGAACTTGCACAGAGTCTCTCAATCTTGAATTCGTATG 499
QY 406 ATTCGCTCTTGTGAGTTTCAATCATTCGAATCTGTCTGGGCTTGTGTGCA 465
Db ATTCGCTCTTGTGAGTTTCAATCATTCGAATCTGTCTGGGCTTGTGTGCA 559
QY 466 TATAGAGATGCGAAGAGATGAGGTTTGTGAAAGCCCTTCTGTGTATGATACC 525
Db TACCGAGATGCGAGGGTCCGCTTCCGCTTTCAGAAAGCCCTTCTGTGTATGATACC 619
QY 526 ATTCGCTTATGCTTCAATAGAGTTGTTTCTGCAAAAACCTAGAGTATATTTTTC 585
Db ATTCGCTTATGCTTCAATAGAGTTGTTTCTGCAAAAACCTAGAGTATATTTTTC 679
QY 620 ATTCGCTTATGCTTCAATAGAGTTGTTTCTGCAAAAACCTAGAGTATATTTTTC 679
QY 586 ACCTGTGCACTCAGAACTCTCCGTTTCTCAAGATCCTCCGATGCTGATGACGCA 645
Db ACCTGTGCACTCAGAACTCTCCGTTTCTCAAGATCCTCCGATGCTGATGACGCA 739
QY 646 AGGGAGGCACTTGGAAATTAATCTGCTGCTTCAAGTCTGATGCAAGCAAGAAATTAATC 705
Db CCGGGGCGGCACTGGAAGCTGCTGCTGCTGATGCAAGCAAGAAATTAATC 799
QY 706 ACAGCTTGTGATAGAGATTTTGTGTTTCTTATTTTCTGCTTCTGCTGCTGCTGCTG 765
Db ACCGCTGTGATAGAGATTTTGTGTTTCTTATTTTCTGCTTCTGCTGCTGCTGCTG 859
QY 766 GAAAGAGATGCCAATAAAGATTTTCTATATGAGATGCTCTGCTGCTGCTGCTGCTG 825
Db GAAAGAGATGCCAATAAAGATTTTCTATATGAGATGCTCTGCTGCTGCTGCTGCTG 919
QY 826 ACATTTACAACTATTTGGCTATGAGAACAAATCTCCCTTAACTTGGCTGGAGATTCCT 885
Db ACATTTACAACTATTTGGCTATGAGAACAAATCTCCCTTAACTTGGCTGGAGATTCCT 979
QY 920 ACATTTACAACTATTTGGCTATGAGAACAAATCTCCCTTAACTTGGCTGGAGATTCCT 979
QY 886 TCTGCAAGCTTGTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Db GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
QY 946 TCAAGTTTGTGATTAAGATCAAGAACAAACCGGCGAGAAACATTTGAGAAAGAG 1005
Db TCGGGCTTTGGCTTGAAGGTTCAGAGACGACACCGGCGAGAAAGATTTGAGAAAG 1099
QY 1006 AACCCAGCTGCACTCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065
Db ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
QY 1066 GTTTCATTTGCAACTGGAAGCACACTTGAAGCCCTTGAACCTGAGC----- 1116
Db GCTTACTGACAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
QY 1117 CCTACCAAGAAAGAACAGGAGGAGATCAAGAGCTA----- 1161

Db 1220 GCCCTCTGTTTAAAGACGTCGCAACGGGCGGCAATGGGGGCTTACGGCCCTGAGGTC 1279
QY 1162 ----- 1161
Db 1280 CGGCGGCGCGGTACCCGACGAGACACCTCCGTTACCCGCGCTTGCACCTGAC 1339
QY 1162 -----AGTTTAAAGACCGA 1176
Db 1340 CGGCGGCGGACACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
QY 1177 GTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1230
Db 1400 ATCCGATGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
QY 1231 GGTGACAGAGGTCCTCCCAAGACCTGACATCAACCGGAGG--GCACTCCCAAGATG 1287
Db ACAATGCCACCTCCCAAGACCTGACAGGATGAGGAGGACCAAGCCCAAGATG 1519
QY 1288 CAGAAGAGCTGAGCTTCAACGACCGGACCGGCTTCCGCTGCTGCTGCTGCTGCTGCTG 1347
Db CAAGAAGAGCTGAGCTTCAACGACCGGACCGGCTTCCGCTGCTGCTGCTGCTGCTGCTG 1573
QY 1348 TCTCAGCCAAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATGATGAT 1407
Db 1574 -----AAACCCCGGACCTCTGCTGAGATGCTGCTGCTGAGAGATGCTGCTGAGAG 1621
QY 1408 GAAAAAGATGCCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1467
Db GAGAAAGATGCTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1681
QY 1468 ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1527
Db ATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1741
QY 1528 CGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1587
Db CGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1801
QY 1588 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1644
Db GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1861
QY 1645 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1704
Db AGAAGGCGCGGAGAGAGGAG 1921
QY 1705 AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
Db AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1981
QY 1765 GACTGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1824
Db GACTGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2035
QY 1825 TTGGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1884
Db CTGGGCGCTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2095
QY 1885 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1918
Db GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2129

RESULT 7
US-09-177-650-88
; Sequence 88, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE


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; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blaneat, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoef, Valentin K.
; APPLICANT: Leveque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Men-Pin
; TITLE OF INVENTION: KClO4 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105, 058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055, 599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
; US-09-105-058C-22

Query Match      16.7%; Score 511.6; DB 3; Length 2169;
Best Local Similarity 58.2%; Pired. No. 4.3e-143;
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;

QY 73 GGGCTGCTACTGCTGGGCAACCCCGGCGCCACGCTTGCGGCGCGGCTGAGG 132
DB 67 GGGCTTGTGGGGGTGACCCCGGCGCGCCGACTCCAACGCGCGGCTACTCATC 126
QY 133 GAGAGCCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCCTGTGGGAAAGCCGCTCTTAC 192
DB 127 GCGGGCTCCGAGGCCCGCCAAAGCCGCGAGCTTTGAGCAAGCCGCGAGCGGCGCG 186
QY 193 ACGAGTACCGCAAGCTGCGCGCGCAACGTCAAGTACCGCGGGTGAGACTACTATC 252
DB 187 GAGCGCGGGAAGGCCCGGAAGCGCAAGCCTTCTACCGCAAGTGGCAATTTCTCTAC 246
QY 253 AAGCTGTGAGAGAGACCCCGCGCTGGGCTTCACTCAACGCTTCTGTTTCTCTT 312
DB 247 AAGCTCTAGAGGCGCGCGCGCGCTGGGCTTCACTCAACGCTTCTGTTTCTT 306
QY 313 GCTTTGCTGCTGCTGATTTTGTAGGCTTTCTACCATCCCTGAGGACAAATTGGCC 372
DB 307 GCTTTCTCTGCTTGTGCTTCTTGTGTTTCAACATCAAGAGTACGAAAGAGCTCT 366
QY 373 TCAAGTTGCTCTGATTCCTGAGTTCGATGATTCGCTTTGCTTGGAGTTTCAATC 432
DB 367 GAGGGGGCCCTCAATCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 426
QY 433 ATTGAATCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
DB 427 GTGAGGATCTGCGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
QY 493 TTTGCTGCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
DB 487 TTTGCTGCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
QY 553 GTTTCTGCAAAAAGCTGATATTTTGTGCAAGCTGCTGCTGCTGCTGCTGCTGCT 612
DB 547 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 613 CTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
DB 607 TTCAAAATCTTGGGATGATTCGATGATGATGATGATGATGATGATGATGATGAT 666
QY 673 TCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
DB 667 TCGGTATCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
QY 733 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
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DB 727 CTCATCTGCGCTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 793 ACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
DB 787 ACCTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 853 AAAAATCCCTTAAGCTTGGTGGGAAAGTCTTCTGCAAGCTTGGCTGCTGCTGCTGCT 912
DB 847 AAGTACCTCAGACCTGGAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
QY 913 TCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
DB 907 TCGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 973 CAACACCGCAGAAACCTTTGAGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1032
DB 967 CAGCATGCGCAAAACCTTTGAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1026
QY 1033 GTTTGCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
DB 1027 GCTGGAAGATTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
QY 1064 -----CTGTTTCAATGCAACCTGGAAGCCTGGAAGCCTGGAAGCCTGGAAGCCT 1107
DB 1087 TACGAGCGGACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 1108 ACCTGAGCCCTAACGAA-----AAGAAAGGGA 1140
DB 1147 CTGCTGGAAGATCTCAAGAGCAAAATCTGATCTACCTTCAAGAAAGGACACGCAAG 1206
QY 1141 GCATCAAGAGCTCAGAACTTAAGTTTAAAGAGCG--TCCGATGCTGCTGCTGCTGCT 1197
DB 1207 CCATCAAGAGCTCAGAACTTAAGTTTAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
QY 1198 GGCAGAGTATTAAGAGCCGCAAGGCTGATGATGATGATGATGATGATGATGATGAT 1257
DB 1267 GCTGCCAAGGAAAGGAGGCTCTCCCAAGCGGACGAGCGGCTGCTGCTGCTGCTGCTGCT 1326
QY 1258 ATCAAGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
DB 1327 CAGAGCTTGAATGACAGCCGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
QY 1318 CGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
DB 1387 CCGACAGCGCAGGCTTCCGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 1378 AAGCGCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
DB 1447 C---TCCCTGGGAGGACATGTAAGGACAAAGAGCTGTAAGGAGTTTGTGACT 1503
QY 1438 GAAAGCTTCAACCCCTGAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1497
DB 1504 GAAAGCTTCAACCCCTGAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1563
QY 1498 GTTGAAGGAGGATTAAGAAACRTAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1557
DB 1564 GTATCTAAGCGAAAGTTCAAGAGAGTCTGCGCCATTAAGTAAAGTAAAGTAAAGTAA 1623
QY 1558 CAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
DB 1624 CAGTACTCGGCTGGAACCTTGAATATGTTGTCCGATCAAGAGCTGCAAGAGTG 1683
QY 1618 GATCAATTTCTGGAAGGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1677
DB 1684 GACCAAGATTTGGGGCGGGCCCAAAATTAAGGATTAAGG---TCCGACCAAGGCCCA 1740
QY 1678 GCAGAAATGAGACCAAGATCTCAGTATGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737
DB 1741 GCGGAAAGGAGCTGCGGAAAGCCCAAGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1738 CAGGTACAGTCAATGAATCAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1791
DB 1801 CAGGCTTGTCCATGGAAGAAAGCTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
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RESULT 9
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303
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Query Match      16.6%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 5.4e-143;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY      1630 GGAAGAGGCAATCATCATGATGAAGAGCGAGAGAAATTAACAGCAGACATGAG 1689
DB      1  GGAAGAGGCAATCATCATGATGAAGAGCGAGAGAAATTAACAGCAGACATGAG 60
QY      1690 ACCACAGAGATCTCGTATGCTCGGTGCGGTGCTAAAGTTGAAAACAGGTACGTC 1749
DB      61  ACCACAGAGATCTCGTATGCTCGGTGCGGTGCTAAAGTTGAAAACAGGTACGTC 120
QY      1750 ATGAATCAAGCTGAGTCTGCTACTAGACATCTATCAACAGGTCCTTGGAAAGCTCT 1809
DB      121  ATGAATCAAGCTGAGTCTGCTACTAGACATCTATCAACAGGTCCTTGGAAAGCTCT 180
QY      1810 GCCTCAGCCCTGCTTGGCTTCATTCAGTCCACCTTTTGATGTGAACAGCATCT 1869
DB      181  GCCTCAGCCCTGCTTGGCTTCATTCAGTCCACCTTTTGATGTGAACAGCATCT 240
QY      1870 GACTATCAAGCCCTGTGATATGCAAGATCTTTGGGTTCCGCAAAACAGTGGCTGC 1929
DB      241  GACTATCAAGCCCTGTGATATGCAAGATCTTTGGGTTCCGCAAAACAGTGGCTGC 300
QY      1930 TTATCCAGATCACTAGTSCCAACATCTGAGAGGCTGACAGTTCATTCTGACGCCAAT 1989
DB      301  TTATCCAGATCACTAGTSCCAACATCTGAGAGGCTGACAGTTCATTCTGACGCCAAT 360
QY      1990 GAGTTGAGTCCGACACTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2049
DB      361  GAGTTGAGTCCGACACTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 420
QY      2050 GAGCCAAATTAGTCAAGGAGTGGCTGAGAGTGGGCGCAACCAACCTTGCACCAACCA 2109
DB      421  GAGCCAAATTAGTCAAGGAGTGGCTGAGAGTGGGCGCAACCAACCTTGCACCAACCA 480
QY      2110 ATTAATACGCAACCAAGCAGAGCCCAACAACTTTACAGATC 2154
DB      481  ATTAATACGCAACCAAGCAGAG--CCCAACAACTTTACAGATC 524
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RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
```

```
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence;Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1
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Query Match      15.2%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 1.9e-129;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;
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QY      199  AGCCAGAGCTCGCGCGCAAGTCAAGTACCGCGGTCGAGACTTACTGTCAACGTCG 258
DB      13  RGSNMSCMSYSAAGMGAACGCCWMSYACCGSMKMSYSCARAMTTMTCTACACACYS 72
QY      259 CTGAGAGAGCCCGCGGCTGAGGCGTCTATCAACAGCGTTTGTTCTCTCTGTTT 318
DB      73  CTGAGAGAGCCCGCGGCTGAGGCGTCTATCAACAGCGTTTGTTCTCTCTGTTT 132
QY      319 GATTCCTGATATTTGTCTGATTTTCTTCAATCCCTGAGCACACAAATTTGCGCTCAAGT 378
DB      133  KSSTCGTBRKTGKCTGTS -YKWCACAMWTCAAGAGTAYGAGAMRKXTCBGRBRS 191
QY      379 TGCCCTTGATTCCTGAGTGTGATGATTTGTCTGCTTTGTTGAGTTTATCATCTTGA 438
DB      192  KSSCTTYWSMTMYTGAAYMKRKCVATYKTSRTVYGGHGBGAGTWKYKVTGMGR 251
QY      439 ATTCGTCTGCGGGTGTGCTGTGTCATATAGAGATGAGCAAGAACTGAGTTTGTCT 498
DB      252  ATTCGTCTGCGGGTGTGCTGTGTCATATAGAGATGAGCAAGAACTGAGTTTGTCT 311
QY      499 CGAAAGCCCTTCTGTATATAGATACATTTGTTTATCGCTTCAATGACAGTTGTTCT 558
DB      312  MGAARCCVCTSTGRTGATGAVATCWTGKTGTSATYGGCTCTVRKSCDPTGSKCY 371
QY      559 GCAAAACTCAGGATATATTTTGGCCAGCTCTGACATCAGAAGTCTCCGTTTCTACAG 618
DB      372  GYBGGHMMCCARGGCAAGTYTYKGCYACVTCY---CTBCRACAGCTTCGTTCTYR 428
QY      619 ATCTCCGATGATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
DB      429  ATYTRCGSATGMSGCBATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
QY      679 GTTATGCTCAGCAGCAAGAAATTAATCAACAGCTTGTATAGATATTTTGTGTTTAT 738
DB      489  RTCTRTGTCACAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
QY      739 TTTTGTCTTTCTTGTCTATCTATCTGATGATGATGATGATGATGATGATGATGAT 798
DB      549  CTKCYTCTRTTYCTKTSYCTACYTGTGATGATGATGATGATGATGATGATGATGAT 608
QY      799 GAGATGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 858
DB      609  GGRATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
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Qy	CCCCCTA	CTGGGCGGGGAAAGTGGCTTTCGCAAGCTTGGACGCTTGGCATTTCTTTC	918
Db	CCYAAAC	CTGTGRAMGSGMGKCTSTHDCVCAACTTWCCTWATYGGYGTCTCVTT	728
Qy	TTTGCAC	TCTCCGCGCGGCGCATTCCTGGCTCAAGTTTTCATTAATAAGTACAAGAACAC	978
Db	TTTGCGB	CTCKCWMGCDGSCATYYTGGGRCTCYGGSYTKGCCCTSAARGTBCAAGACARAY	788
Qy	CGCCAGAA	AAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACTCATTCAGTGTGTTGG	1038
Db	MGKAPARA	CACTTTGAGAAARMGGMGAABCCDGDGCMGBBTSATYCAAGKCKCTGG	848
Qy	CGTAGT	TAACGACGCTGA	1055
Db	AGRTWY	TAYTACGYACVAA	865

Db 1707 TGACWTCCTCATGMAAGACATGATCCCTCCCTWMAAGCGTCGCATCCGAGCTGTCAAGAT 1766
Qy 1485 TATGAATTCATGATGTCGCAAAACGGAAGTTTAAAGAAACCTTACGTCCTATGATGTAAA 1544
Db 1767 TCACAGCTCCGCTCTATATATAAAAAAGTTCAAGAGAGACGTTGAGGCTTTATGATGTGAA 1826
Qy 1545 AGATGTCATGAAACATATTTCTGTGTATCTGATCTGACATGTTGTGTAGAAATTAAAGCCT 1604
Db 1827 AGATGTGATTTGACAGATATTTCCGCGGACATCTTGACATGCTTTCCAGAGATTAAGTACCT 1886
Qy 1605 TCMAACACGTTGATCAATTCT 1628
Db 1887 ACAGACAAGATGATATGATTTT 1910

RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Dwoiczky, Steven
; APPLICANT: Griskoif, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Men-Pin
; TITLE OF INVENTION: KENO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 15.0%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 1.1e-127;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

Qy 22 GAGTGGGCGCGGGGCGAGGCTGCTGTAAGTCTGGGCGAGCGCCGACGAGGGGCGACGCGCTGCTA 81
Db 43 GCGGCGGCGGCGCGGCGGCGACGAGAGCGGAAAGTGGGCTGGCGCGCGCGACGCTGGAGCAA 102
Qy 82 CTGCTGGGCAACCGCGCGGCGCAACGCTTGGTGGCGGCGGCGGTGGCTTGAAGGAGAGCCGC 141
Db 103 GTACACTTGGCGCTCGGGGCGGAGCGCAAAAGACGGAACCTGCTGCTGAGAGGGCGGC 162
Qy 142 CGGGGCGACGAGGGGCGCGGATGAGCTGTGGGGAGACCGCTCTCTTACACGAGTAGC 201
Db 163 GCGCGGCGAGAGGGGCGAGGAGAGACCGCGAGGGGCGATGGGCTCTGCGCAAGACCCCG 222
Qy 202 CAGAGCTGCC-----GCGCGAACGTCAAGTACCGGCGGGGTGAGAACTACCTGTAC 252
Db 223 CTGAGCGCGCCGACGTCAAGAGAAACACGCGCAAGTACCGGCGGCAATCCAAACTTGTGATCTAC 282
Qy 253 AACGTGCTGAGAGACCCCGCGGCTGGGCGTTTCATTCACGCGTTTCGTTTTCTCCTT 312
Db 283 GAGCGCTTGAAGAGACCGGGGGCTGGGCGCTCTTACACGCGTTGATGTTCTGATTT 342
Qy 313 GTCTTTGTTGCTTGAATTTTGTCAAGTGTCTTTCACCATCCCTGAGACACAAATTTGGCC 372
Db 343 GTCTGGGGGTGCTGTGATTTCTGGCTGTCTGACCACTTCAAGAGATGAGACTGTCTCG 402
Qy 373 TCAAGTGGCTCTGTGATCTCTGAGATTCGAGATGATTTGTCTTTGGTTTGAAGTTGATC 432
Db 403 GGAAGACTGGCTTCTGTACTGTGAGACATTTGCTATTTTCATCTTGGAGCCGAGTTTGCT 462

Qy 433 ATTGAATCTGTGCTGCGGGTTTGCTGTGTGATATAGAGATGGCAAGGAAGACTGAGG 492
Db 463 TTGAGGATCTGGGCTGCTGAGATGTTGTGCGATACAAAGGCTGGGGCCGAGCTGAAG 522
Qy 493 TTTGCTCGAAAGCCCTTCTGTGTATATAGATACATTTGTTCTTATCGCTCAATAGACAGTT 552
Db 523 TTTGCGAAGAAAGCCCTGTGTGATGTGAGACATCTTTGTGTGATTTGCTGTGCGAGTG 582
Qy 553 GTTTTTCGAAAAACTCAGGGTAAATTTTGGCAGGTCTGCACTCAGAAGTCTCCGTTTC 612
Db 583 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCACT--CCCTCGAAAGCTGTGGCTTC 639
Qy 613 CTACAGATCTCCGCGATGCGGATGAGACGGAAGGGAGGACATGGAATTAATTCAGGT 672
Db 640 CTGCAGATCTGCGGATGCTGCGGATGAGACCGGAGAGGTGACCTGGAAGCTTTCTGGCG 699
Qy 673 TCAGTGTATTATGCTACAGCAAGGAATTAATCAGAGCTTGTGTACATAGATTTTGGTT 732
Db 700 TCAGGCATCTGTGCGCACAGCAAAAGACTCATCAGCGCTGGTACATCGGTTTCTGACA 759
Qy 733 CTATATTTTGTGCTTTCTTCTGTCTATCTGGTGAAGAAAGATGCC----- 777
Db 760 CTGATCTTTCTTCAATTTCTGTCTACCTGTGGAAGAAAGCTCCAGAGGTGATGCA 819
Qy 778 -----AATAAGAGTTTCTACATATGAGATGCTCTGTGGGGCACA 822
Db 820 CAAGAGAGAGATGAAGAGAGTTTGAAGCTGTGAGATGCTGTGTGGGGCCCTG 879
Qy 823 ATTACATTGACAACTATTGGCTATGAGACAAACCTCCCTTAATCTGCTGGGAAAGATTG 882
Db 880 ATCACTATGCGCACCATTTGGCTATGAGACAAACCAACCAAGCGTGGAAAGGCGCTCG 939
Qy 883 CTTCCTGAGGCTTTGCACTCTTGGCAATTTCTTCTTGTGACCTTCCGCGGCAATCTT 942
Db 940 ATTGCGGCACTTTCTTAAATTTGGCTCTCTTTTGTGCTTCCAGCGGCGATCTCG 999
Qy 943 GCGTCAGGTTTGTGCTTAAAGTACAAAGAACACCGCCGAAACATTTGAGAAAAA 1002
Db 1000 GGGTCGGGGCTGGCCCTCAAGGTGAGAGACACCGCTGAGAGACATTTGAGAAAAAG 1059
Qy 1003 AGGAACCCAGCTGCCAATTCATTCAGTGTGTGGCGTGAATTCGACCTGATAGAAA 1062
Db 1060 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCTGAGAGTATTTAGTACCAACCCCAAC 1119
Qy 1063 TCTGTTTCATTTGCAACTGTGAAGCCACATTTGAAGGCTTGCACACTGCAAGCCCTACC 1122
Db 1120 AGGATTAAGCTGTGGCGACATGAGATTTTATGAAATGATGCTCTTTTCTTTCTTC 1179
Qy 1123 AAGAAAGAAACAAAGGAGAGCATCAAGCAGTCAAGCTTAAGTTTAAAGAGCAGTGGCG 1182
Db 1180 AGGAAGAAACAGCTGAGAGGAGCATCCAGCCAAAGATGGGGCTCTTGGATGGGGTTGGC 1239
Qy 1183 ATGCTAGCCCGAAGGGGCGAAGATTTAAAGCCGACAGACCTCAGTAGTGAACAGAGG 1242
Db 1240 CTTCCTAATCTCGTGTAGCAATTAATA-----AGGAAAGCTATTT 1281
Qy 1243 TCCCCAAGCAACGACATCAAGCGGAGGCGAGTCCACCAAGTGCAGAAAGCTGAGAGC 1302
Db 1282 ACCCTCTGAATGTAGATGCCATAGAAAGAAAGTCTTTTAAAGAACAAAGCTGTGTGGC 1341
Qy 1303 TTCAACGACGAAACCGGCTTCGCGCCCTGCGTGGCGCTCAAAAGTTCTCAGCCAAACCA 1362
Db 1342 TTTAAACATTAAGAGCGTTTCGCGACGCGCTTCGCGATGAAGAGCT-----AGCCTTTC 1395
Qy 1363 GTGATAGATGCTGACACAGCCCTTGGCATGTATGTATATGATGAAAAAGATGCCAG 1422
Db 1396 TGGCAGAGTTCTGAAGATGGCGGAGCAGGTGACCCCATGGCGGAAAGAGAGGGGCTATGGG 1455
Qy 1423 TGTGATGATCAGTGAAGAGACCTACCCGACCACTTAATAACGTGATTTGAGCTATCAGA 1482
Db 1456 AATGACTTCCCATGGAAGACATGATCCCAACCTGAAGGCGCGACTCGAGCCGCTCAGA 1515

QY 1123 AAGAAAGCAAGGGGAGCATATACAGATCAGAGCTAACTTTAAGAGCGAGTGCCG 1182
DB 1252 AAGAAAGCAAGGGGAGCATATACAGATCAGAGCTAACTTTAAGAGCGAGTGCCG 1311
QY 1183 ATGGCTAGCCCGGAGGGGCGAGATATTAAGAGCGCAAGAGCCCACTAGGTGACAGAGG 1242
DB 1312 CTTTCTTAATCTCTGTGTAGCACTACTA-----AGAAAGCTAATTT 1353
QY 1243 TCCCAAGACCGACATCAAGCCGAGGGGAGTCCCAAGAGTGAAGAGAGCTGAGC 1302
DB 1354 ACCCTCTGAATGTAGTATGATGCAAGAAAGTCTTTTAAGAACCAAGAGCTGTGGC 1413
QY 1303 TTGAAGACCGAAGCCGCTCCGAGCCCTGCTGCTGCTCAAAAGTTCTACCAAAACA 1362
DB 1414 TTAAACAAATTAAGAGGCTTCCCAAGGCTTCCGATGAAGCCCT-----ACGCTTTC 1467
QY 1363 GTGATGATGCTGACAGCCCTTGGACATGATGATATGATGATAAAGAGATGCCAG 1422
DB 1468 TGGCAAGTCTTAAGATGCGGAGACAGGTGACCCCAAGGCGGAGAGAGGCTATGAG 1527
QY 1423 TGTATGATCAAGTGAAGACCTCACCCCACTTAAACCTGTCAATTCAGCTATCAGA 1482
DB 1528 AATGACTTCCCATCGAAGACATGATCCCACTGAAGGCGGCATCCGAGCCGTCAAG 1587
QY 1483 ATTATGAATTTATGTTGCAAAACGAAAGTTTAAGAAACRTTACGTCATATGATGA 1542
DB 1588 ATTCTCAATTCGCTCTTATTAATAAAATTCAGAGAGCTTTGAGGCTTACGATGTG 1647
QY 1543 AAGATGCTATTAACATATTTCTGCTGCTCATCTGACATGTTGATGAATTAAGC 1602
DB 1648 AAGATGCTATTAAGAGATTTCTGCGGAGCATCTGACATGCTTTCCAGATTAAGTAC 1707
QY 1603 CTTCAACAACGCTGTTGATCAATTC 1628
DB 1708 CTTCAAGACGAATATGATATTT 1733

RESULT 14
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006f6
; LOCATION: 486, 510, 552, 573
; OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 14.7%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 1,5e-125;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

QY 1630 GAAAAAGGCAATCATCATATAGAGAGCGGAGAAATAACAGCAGAACTGAG 1689
DB 1 GAAAAAGGCAATCATCATATAGAGAGCGGAGAAATAACAGCAGAACTGAG 60

QY 1690 ACCACAGACATCTCATATGCTGCTGCGGTGCTCAAGTTGAAAAACAGGTACATCC 1749
DB 61 ACCACAGACATCTCATATGCTGCTGCGGTGCTCAAGTTGAAAAACAGGTACATCC 120
QY 1790 ATAGAAATCCAGTGTGACTGCTTACTATACATCTTCAACAGTCTTCCGAAAGCTCT 1809
DB 1221 ATAGAAATCCAGTGTGACTGCTTACTATACATCTTCAACAGTCTTCCGAAAGCTCT 180
QY 1810 GCTCAGCCCTGCTTGTGCTTCAATTCAGTTCACACCTTTTGAATGTAAGACATCT 1869
DB 181 GCTCAGCCCTGCTTGTGCTTCAATTCAGTTCACACCTTTTGAATGTAAGACATCT 240
QY 1870 GACTATCAAGCCCTGTGATAGCAAGATCTTGTGCTTCCGACAAACAGTGGCTGC 1929
DB 241 GACTATCAAGCCCTGTGATAGCAAGATCTTGTGCTTCCGACAAACAGTGGCTGC 300
QY 1930 TTATCAGATCAACATAGTGGCAACATCTCGAGAGCCCTGAGTTTATCTGACGCAAT 1989
DB 301 TTATCAGATCAACATAGTGGCAACATCTCGAGAGCCCTGAGTTTATCTGACGCAAT 359
QY 1990 GAGTTCAGTGGCCAGACTTCTACGCGCTTACGCTTACCTATGACAGTCAAGCAACAG 2049
DB 360 GAGTTCAGTGGCCAGACTTCTACGCGCTTACGCTTACCTATGACAGTCAAGCAACAG 417
QY 2050 GTGCAATTAATGTCAAAGGATGCTCAGCAGTGGCAGCCACCAACCATTTGCAACCA 2109
DB 418 GTGCCAA-TAGTCAAAAGGATGCTCAGCAGTGGCAGCCACCAACCATTTGCAACCA 475
QY 2110 ATTAATAGGGACCCCAAGCCAGAGCCCAACACTTACAGATCCACCTCTCT 2165
DB 476 ATTAATAGGGACCCCAAGCCAGAGCCCAACACTTACAGATCCACCTCTCTCT 531

RESULT 15
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaier, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

Query Match 13.8%; Score 425; DB 3; Length 3287;
Best Local Similarity 64.7%; Pred. No. 8.3e-117;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

QY 73 GAGCTGCTACTGCTGGGACACCGGCGCACGCTTGTGCGGGCGGCTGTGAGG 132
DB 127 GAGCTGCTGAGGCTGTGATCCCGGCGCGCCGACATCTCACCCGAGAGCGGCTGTGATC 186
QY 133 GAGAGCCCGCGGCGCAAGCAGAGGCGCCGATGAGCTTGTGGAGAACCGCTCTTAC 192
DB 187 GCGGCTCTCGAGGCGCCCAAGCGGCGAGCATCTCAGCAAAACCTCGCGCGGCGCGG 246
QY 193 ACGAGTACCGAGAGTGGCGGCGCAAGTCAAGTACCGCGGCGGCGAGAACTACTTAC 252

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QY 1 GGCAGCGGATGAAAGATGTGAGTGGGCGGGGAGGAGTGTCTGTAACCTCGAGGCC 60
Db 1 GGCAGCGGATGAAAGATGTGAGTGGGCGGGGAGGAGTGTCTGTAACCTCGAGGCC 60
QY 61 GCCAGGGGGAGCGGCTGTCTACTGTCTGGGCAACCCGGCGGCGCACGCTGTGTGGCGGCG 120
Db 61 GCCAGGGGGAGCGGCTGTCTACTGTCTGGGCAACCCGGCGGCGCACGCTGTGTGGCGGCG 120
QY 121 GGTGCGCTGAGGAGAGCGCGCGGGGCAAGCAGAGGGGGCCCGAGTGAAGCTGTGGGGAAG 180
Db 121 GGTGCGCTGAGGAGAGCGCGCGGGGCAAGCAGAGGGGGCCCGAGTGAAGCTGTGGGGAAG 180
QY 181 CCGCTCTCTTAAACGAGTACCGAGCTGCGGCGCAACGTCAAGTACCAGCGGGGTGACAG 240
Db 181 CCGCTCTCTTAAACGAGTACCGAGCTGCGGCGCAACGTCAAGTACCAGCGGGGTGACAG 240
QY 241 AACTACTCTGTAACAAGTGTGAGAGAACCCCGGCGCTGGGCGTTCACTTACACGCTTTC 300
Db 241 AACTACTCTGTAACAAGTGTGAGAGAACCCCGGCGCTGGGCGTTCACTTACACGCTTTC 300
QY 301 GTTTTCTCCTGTCCTTGGTGTGATTTGTGAGTGTGTCAGTGTGTTCTACATCCCTGAGAC 360
Db 301 GTTTTCTCCTGTCCTTGGTGTGATTTGTGAGTGTGTCAGTGTGTTCTACATCCCTGAGAC 360
QY 361 ACAAAATTTGGCTCAAGTGTGCTTGTATCTGAGATTCGTGATGATGATGATGATGATGAT 420
Db 361 ACAAAATTTGGCTCAAGTGTGCTTGTATCTGAGATTCGTGATGATGATGATGATGATGAT 420
QY 421 TTGGAGTTCACTTGTGAATCTGTGTGGGTTGCTGTGTGCGATGTAGAGATGGCAA 480
Db 421 TTGGAGTTCACTTGTGAATCTGTGTGGGTTGCTGTGTGCGATGTAGAGATGGCAA 480
QY 481 GGAAGACTGAGGTTTCTGAAAGCCCTTGTGTATAGATACATGTTGCTTATCGCT 540
Db 481 GGAAGACTGAGGTTTCTGAAAGCCCTTGTGTATAGATACATGTTGCTTATCGCT 540
QY 541 TCAATGACAGTGTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAACGTCGACATCAGA 600
Db 541 TCAATGACAGTGTGTTCTGCAAAAACCTCAGGGTAATATTTTGGCAACGTCGACATCAGA 600
QY 601 AGTCTCCGTTTCTTAACAGATCTCTCCGAGTGTGCGGATGAGACCGAAGGGAGGCACTTGG 660
Db 601 AGTCTCCGTTTCTTAACAGATCTCTCCGAGTGTGCGGATGAGACCGAAGGGAGGCACTTGG 660
QY 661 AAATTACTGGGTTCACTGTGTTATGCTCAACAGCAAGAAATTAATCAAGCTTGTATGAT 720
Db 661 AAATTACTGGGTTCACTGTGTTATGCTCAACAGCAAGAAATTAATCAAGCTTGTATGAT 720
QY 721 GGAATTTTGGTTCTTAATTTTTCGTTTCCTTGTCTATCTGTGTAAGAAAGATGCAAT 780
Db 721 GGAATTTTGGTTCTTAATTTTTCGTTTCCTTGTCTATCTGTGTAAGAAAGATGCAAT 780
QY 781 AAAAGTTTTTCTAACAATGACAGATGCTCTGTGTGGGCAACAATTAATGACAATATT 840
Db 781 AAAAGTTTTTCTAACAATGACAGATGCTCTGTGTGGGCAACAATTAATGACAATATT 840
QY 841 GGCATGAGAGCAAAACCTCCCTAATGCTGTGGGAAAGTGTCTTCTGACAGGCTTTGCA 900
Db 841 GGCATGAGAGCAAAACCTCCCTAATGCTGTGGGAAAGTGTCTTCTGACAGGCTTTGCA 900
QY 901 GTCTTGGGATTTCTTTTCTTGCATCTCTGCGGCAATCTTGGCTCAGGTTTGCATTTA 960
Db 901 GTCTTGGGATTTCTTTTCTTGCATCTCTGCGGCAATCTTGGCTCAGGTTTGCATTTA 960
QY 961 AAAAGTCAAGAACACACCGCCAGAAACCTTTGAGAAAAGAAAGAACCCAGCTGCAAC 1020
Db 961 AAAAGTCAAGAACACACCGCCAGAAACCTTTGAGAAAAGAAAGAACCCAGCTGCAAC 1020
QY 1021 CTCATTCACTGTGTGTGGGTGATTAACGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1080
Db 1021 CTCATTCACTGTGTGTGGGTGATTAACGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1080
QY 1081 TGAAGCCCACTTGAAGGCTTGGCACTGTGACGCTTACCCAGAAAAGAACAGGGGA 1140
Db 1081 TGAAGCCCACTTGAAGGCTTGGCACTGTGACGCTTACCCAGAAAAGAACAGGGGA 1140
QY 1141 GCATCAACAGTCAAGAACTTAAGTTTAAAGAGCGAGTGGCATAGCCCCAGGGGC 1200
Db 1141 GCATCAACAGTCAAGAACTTAAGTTTAAAGAGCGAGTGGCATAGCCCCAGGGGC 1200
QY 1201 CAGATATTAAGAGCGCAAGGCTCAGTAAGTGAACAGAGGTCCCAAGCCAGCAATC 1260
Db 1201 CAGATATTAAGAGCGCAAGGCTCAGTAAGTGAACAGAGGTCCCAAGCCAGCAATC 1260
QY 1261 ACAGCCAGGGGAGTCCCAACCAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
Db 1261 ACAGCCAGGGGAGTCCCAACCAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
QY 1321 TTCCGGCCCTGCGTGGCTCAAAAGTTCTCAGCCCAAAACCGATATGATGCTGACACA 1380
Db 1321 TTCCGGCCCTGCGTGGCTCAAAAGTTCTCAGCCCAAAACCGATATGATGCTGACACA 1380
QY 1381 GCCCTTGGCACTGATGATGATATGATGATAAGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 GCCCTTGGCACTGATGATGATATGATGATAAGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 GACCTCACCCCACTTAAATCTGTCAATTCGAGCTATCAGAAATTAATTAATTCATGTT 1500
Db 1441 GACCTCACCCCACTTAAATCTGTCAATTCGAGCTATCAGAAATTAATTAATTCATGTT 1500
QY 1501 GCAAAACGGAAGTTTAAGAAACCTTAAGTCAATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 GCAAAACGGAAGTTTAAGAAACCTTAAGTCAATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 TATTCGTGTCATCTGACATGTTGTGTAATTAAGGCTTCAAAACGTTGAT 1620
Db 1561 TATTCGTGTCATCTGACATGTTGTGTAATTAAGGCTTCAAAACGTTGAT 1620
QY 1621 CAATTTCTTGAAGGCAATCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CAATTTCTTGAAGGCAATCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 GAACTAGACCAACAGATCTCAGTATGCTCGGTGGGTTGATGATGATGATGATGATGATGAT 1740
Db 1681 GAACTAGACCAACAGATCTCAGTATGCTCGGTGGGTTGATGATGATGATGATGATGATGAT 1740
QY 1741 GTACAGTCAATGATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 GTACAGTCAATGATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAAGGCTCTGAGCCCTGCTTGGCTTCAATTCAGTTCCCACTTTGAAATGTAA 1860
Db 1801 AAAGGCTCTGAGCCCTGCTTGGCTTCAATTCAGTTCCCACTTTGAAATGTAA 1860
QY 1861 CAGACATCTGATCAAGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 CAGACATCTGATCAAGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1921 AGTGCTGCTTATCAAGATCACTAGTGCACAACTCTGAGAGGCTCAGTTCTTGTG 1980
Db 1921 AGTGCTGCTTATCAAGATCACTAGTGCACAACTCTGAGAGGCTCAGTTCTTGTG 1980
QY 1981 ACGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
Db 1981 ACGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
QY 2041 GCAACAGAGGTCATTAAGTCAAGAGGCTCAGAGTGGAGGCAACCAACCACTT 2100
Db 2041 GCAACAGAGGTCATTAAGTCAAGAGGCTCAGAGTGGAGGCAACCAACCACTT 2100
QY 2101 GCAAAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Db 2101 GCAAAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
QY 2161 CCTCTCCAGGCAATCAAGCATCTGCGCAAGGCAAGAACTTGCACCTTAACCTTGCAGGC 2220

[illegible]

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RESULT 2
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661.629

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; CURRENT FILING DATE: 2003-09-15
;
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;
; LENGTH: 3137
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

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Query Match	99.0%;	Score 3040.4;	DB 19;	Length 3137;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 3041;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
OY	10	ATGAAGATGTGAGTCCGGCCGGGGGACAGGAGTGTCTGTGAACTCGCGACGCCGACGAGGC	69	
Db	1	ATGAAGATGTGAGTCCGGCCGGGGGACAGGAGTGTCTGTGAACTCGCGACGCCGACGAGGC	60	
OY	70	GACGGCTCTCTACTGCTCTGGGCACCCCGGCGGACACGCTTGATGGCGGCGGTGGCTG	129	
Db	61	GACGGCTCTCTACTGCTCTGGGCACCCCGGCGGACACGCTTGATGGCGGCGGTGGCTG	120	
OY	130	AGGAGAGACCGCCGGGGCAAGCAGAGGGGACCGATGAGCTGCTGGGGAAAGCCGCTCT	189	
Db	121	AGGAGAGACCGCCGGGGCAAGCAGAGGGGACCGATGAGCTGCTGGGGAAAGCCGCTCT	180	
OY	190	TACACGATGACAGAGCTGCGGCGCAAGCTCAAGTACCGGCGGGTGCAAACTACCTG	249	
Db	181	TACACGATGACAGAGCTGCGGCGCAAGCTCAAGTACCGGCGGGTGCAAACTACCTG	240	
OY	250	TACACGATGACAGAGACCCCGGGCGGTACCTACACAGCGTTTGCTTTCTC	309	
Db	241	TACACGATGACAGAGACCCCGGGCGGTACCTACACAGCGTTTGCTTTCTC	300	
OY	310	CTTGCTTTGGTTCCTGATTTTGTCTAGTGTCTTCTACATCCCTGAGCACACAAATTG	369	
Db	301	CTTGCTTTGGTTCCTGATTTTGTCTAGTGTCTTCTACATCCCTGAGCACACAAATTG	360	
OY	370	GCCTCAGTGGCCCTCTTGATCTCTGGAGTCTGGATGATTTGTCCTTTGGTTGGAATTC	429	
Db	361	GCCTCAGTGGCCCTCTTGATCTCTGGAGTCTGGATGATTTGTCCTTTGGTTGGAATTC	420	
OY	430	ATCATTCGAATCTGGTCTGGGGGTTCGTGTGTGTCATATAGAGATGGCAAGAACTG	489	
Db	421	ATCATTCGAATCTGGTCTGGGGGTTCGTGTGTGTCATATAGAGATGGCAAGAACTG	480	
OY	490	AGGTTTGTGAAAGCCCTTCTGTGTATAGATCCATTTGTTCTTATGCTTCAATGCA	549	
Db	481	AGGTTTGTGAAAGCCCTTCTGTGTATAGATCCATTTGTTCTTATGCTTCAATGCA	540	
OY	550	GTGTGTTCTGGAAGAACTCAGGGGTATATATTTTGGCAGCTGACACAGAGCTCCGT	609	
Db	541	GTGTGTTCTGGAAGAACTCAGGGGTATATATTTTGGCAGCTGACACAGAGCTCCGT	600	
OY	610	TTCTCTACAGATCTCTCCGATGCTGCGCATGAGCCGAAGGGAGGCACTTGGAAATTA	669	
Db	601	TTCTCTACAGATCTCTCCGATGCTGCGCATGAGCCGAAGGGAGGCACTTGGAAATTA	660	
OY	670	GGTTCAGTGGTTATGCTCACAGGAAGAAATTAATCACACTTGGTATCATAGAGATTTTG	729	
Db	661	GGTTCAGTGGTTATGCTCACAGGAAGAAATTAATCACACTTGGTATCATAGAGATTTTG	720	
OY	730	GTTCCTATTTTTTTCGTTCTTCTTGTCATCTGGTGAAAGAGATGCAATAAGATT	789	
Db	721	GTTCCTATTTTTTTCGTTCTTCTTGTCATCTGGTGAAAGAGATGCAATAAGATT	780	
OY	790	TCTACATATGCAATGCTCTCTGGTGGGGACAATTAATTAAGCAACTATTTGGCTATGA	849	
Db	781	TCTACATATGCAATGCTCTCTGGTGGGGACAATTAATTAAGCAACTATTTGGCTATGA	840	
OY	850	GACAAACTCCCCCTTATGCTGATGGGAAAGATTGTTCTCAGAGCTTTGCATCTCTTGGC	909	

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Db      841 GAAAAAATCTCCCTTAATCTGGCTGGGAAAGATGCTTTCGACAGCTTTGGACCTCTGGG 900
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Db      901 ATTTCTTTCTTTGACATTTCTGCGGCAATCTTGGCTCAGTTTTCATTTAAAGTACA 960
Qy      970 GAAACAACCCGACAGAAACATTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTCAG 1029
Db      961 GAAACAACCCGACAGAAACATTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTCAG 1020
Qy      1030 TGTGTTTGGGTGATTAAGAGCTGATGAGAAATCTGTTCCATTGCAACTTGGAGCCA 1089
Db      1021 TGTGTTTGGGTGATTAAGAGCTGATGAGAAATCTGTTCCATTGCAACTTGGAGCCA 1080
Qy      1090 CACTTGAAGGCTTTGACACCTGACAGCCCTTACCAAGAAAGAACAGGGAGCATCAAG 1149
Db      1081 CACTTGAAGGCTTTGACACCTGACAGCCCTTACCAAGAAAGAACAGGGAGCATCAAG 1140
Qy      1150 AGTCAGAGCTTAAGTTTAAAGAGCGAGTGCATGCTAGCCCAAGGGCCAGATATT 1209
Db      1141 AGTCAGAGCTTAAGTTTAAAGAGCGAGTGCATGCTAGCCCAAGGGCCAGATATT 1200
Qy      1210 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGCAACCGACATCAAGCCGAG 1269
Db      1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGCAACCGACATCAAGCCGAG 1260
Qy      1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAAGCAACCGCTTCCGGCCC 1329
Db      1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAAGCAACCGCTTCCGGCCC 1320
Qy      1330 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACAGCCCTTGGC 1389
Db      1321 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACAGCCCTTGGC 1380
Qy      1390 ACTGATGATGTATGATGATGAAAAAGATGCGAGTGTATGATGATGAGAAAGCTCAGC 1449
Db      1381 ACTGATGATGTATGATGATGAAAAAGATGCGAGTGTATGATGATGAGAAAGCTCAGC 1440
Qy      1450 CCACCACTTAAACCTGCTATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1509
Db      1441 CCACCACTTAAACCTGCTATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1500
Qy      1510 AAGTTTAAAGAAACRTTACGTCCATATGATGTTAAAGATGTCATGACATATTTCTGCT 1569
Db      1501 AAGTTTAAAGAAACRTTACGTCCATATGATGTTAAAGATGTCATGACATATTTCTGCT 1560
Qy      1570 GGTCACTGTGGAACATGTTGTGTAAGAAATTAAAGCCTTCAAAACGCTGTGATCAAAATTTCT 1629
Db      1561 GGTCACTGTGGAACATGTTGTGTAAGAAATTAAAGCCTTCAAAACGCTGTGATCAAAATTTCT 1620
Qy      1630 GAAAAAGGGCAATCATCATAGATAGAAAGAGCCGAGAAAAATTAACAGCAGAACATGAG 1689
Db      1621 GAAAAAGGGCAATCATCATAGATAGAAAGAGCCGAGAAAAATTAACAGCAGAACATGAG 1680
Qy      1690 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC 1749
Db      1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC 1740
Qy      1750 ATAGAATCCAGCTGAGCTGACCTAAGACATCTATCAACAGAGTCCCTTGGAAAGGCTCT 1809
Db      1741 ATAGAATCCAGCTGAGCTGACCTAAGACATCTATCAACAGAGTCCCTTGGAAAGGCTCT 1800
Qy      1810 GCTTCAGCCCTGCTTTGGCTTCAATTCAGATCCCACTTTGAAATGTGACAGACATCT 1869
Db      1801 GCTTCAGCCCTGCTTTGGCTTCAATTCAGATCCCACTTTGAAATGTGACAGACATCT 1860
Qy      1870 GACTATCAAAAGCCCTGTGATAGCAAAAGTCTTTGGGGTCCGCACAAAAACGTGGCTGC 1929
Db      1861 GACTATCAAAAGCCCTGTGATAGCAAAAGTCTTTGGGGTCCGCACAAAAACGTGGCTGC 1920
Qy      1930 TTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTGCAATTCATTTCTGACGCCAAT 1989
Db      1921 TTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTGCAATTCATTTCTGACGCCAAT 1980
Qy      1990 GAGTTCAGAGCCAGACCTTTTACAGGAGCTTACGCTTACATGATGACAGTCAAGCAACAG 2049
Db      1981 GAGTTCAGAGCCAGACCTTTTACAGGAGCTTACGCTTACATGATGACAGTCAAGCAACAG 2040
Qy      2050 GTGCCAATTAATGTCAAAGCGATGGCTCAGCAGTGGAGCCCAACCAATTCGCAACCA 2109
Db      2041 GTGCCAATTAATGTCAAAGCGATGGCTCAGCAGTGGAGCCCAACCAATTCGCAACCA 2100
Qy      2110 ATAAATACGGCAACCCAGCGACAGACCCCAACAACTTTTACAGATCCCACTCTCTCCA 2169
Db      2101 ATAAATACGGCAACCCAGCGACAGACCCCAACAACTTTTACAGATCCCACTCTCTCCA 2160
Qy      2170 GCCATCAAGCATCTGCCAGGCGCAAAAATCTGCACACCTTAAACCTTGACAGGCTTACAGAA 2229
Db      2161 GCCATCAAGCATCTGCCAGGCGCAAAAATCTGCACACCTTAAACCTTGACAGGCTTACAGAA 2220
Qy      2230 AGCATTTCTGACGTACCACTGCTGCTGCTCCTCAAGAAAATGTTCAAGTTGCAAG 2289
Db      2221 AGCATTTCTGACGTACCACTGCTGCTGCTCCTCAAGAAAATGTTCAAGTTGCAAG 2280
Qy      2290 TCAAAATCTCACCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAAAATCTCG 2349
Db      2281 TCAAAATCTCACCAAGGACCGTTCTATGAGAAAAGCTTTGACATGGAGAGAAAATCTCG 2340
Qy      2350 TTGCTGTCTGTCCCATGAGTGCAGAAAGCTTGGCAAAATCTTGTCTGTGCAAAACCTG 2409
Db      2341 TTGCTGTCTGTCCCATGAGTGCAGAAAGCTTGGCAAAATCTTGTCTGTGCAAAACCTG 2400
Qy      2410 ATCAGGTGACCGAGAACTGATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2469
Db      2401 ATCAGGTGACCGAGAACTGATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2460
Qy      2470 GGCAGCCAAAGTTTTTACCCCAAAATGAGGGAATCCAAATGTTTATTAATGATGAAGAG 2529
Db      2461 GGCAGCCAAAGTTTTTACCCCAAAATGAGGGAATCCAAATGTTTATTAATGATGAAGAG 2520
Qy      2530 GTGGTCCCGAAGACAGACAGACACTTTTGTATGTCGCGACCGCAACCTGCGCAGGAA 2589
Db      2521 GTGGTCCCGAAGACAGACAGACACTTTTGTATGTCGCGACCGCAACCTGCGCAGGAA 2580
Qy      2590 GCTGCTTTGATCAGACTCTCTTAAGGACTGAAAGTCAACATCATCTCAGAGCAATTTGT 2649
Db      2581 GCTGCTTTGATCAGACTCTCTTAAGGACTGAAAGTCAACATCATCTCAGAGCAATTTGT 2640
Qy      2650 AAGCAGAGAAAGTACAGATGGCCCTGAGTGTGCTCATGTGCAACCTGAATTAAGTCTT 2709
Db      2641 AAGCAGAGAAAGTACAGATGGCCCTGAGTGTGCTCATGTGCAACCTGAATTAAGTCTT 2700
Qy      2710 CATTTTCTTCCAGGCAATGAGTCTTTTACCATATCATATCATTTGACATGAACTATTCG 2769
Db      2701 CATTTTCTTCCAGGCAATGAGTCTTTTACCATATCATATCATTTGACATGAACTATTCG 2760
Qy      2770 AAAGCCCTTCTAATAAGTTGAAATTTGCAGAATGGGAAAGACITGAAGGCAATTATA 2829
Db      2761 AAAGCCCTTCTAATAAGTTGAAATTTGCAGAATGGGAAAGACITGAAGGCAATTATA 2820
Qy      2830 AGCCCGTAACTTTTAAATGATGAGAAATGCAATGTTTAAAGGATGGCTAAATTTCCAAAGT 2889
Db      2821 AGCCCGTAACTTTTAAATGATGAGAAATGCAATGTTTAAAGGATGGCTAAATTTCCAAAGT 2880
Qy      2890 GCATGACATTTAACCACTCAATTAATGATGATGATGATGATGATTAATAAGCTGAGAAACA 2949
Db      2881 GCATGACATTTAACCACTCAATTAATGATGATGATGATGATGATTAATAAGCTGAGAAACA 2940
Qy      2950 AACACAGCTAATGCTATGGGGTGTATGAAATATGCAAGTTTAAAGTCAATTAAGAAATTTG 3009
Db      2941 AACACAGCTAATGCTATGGGGTGTATGAAATATGCAAGTTTAAAGTCAATTAAGAAATTTG 3000
Qy      3010 ACACGTATTTTGAATTAATGGGAGTAAACACTTCAAAATTTCA 3053
Db      3001 ACACGTATTTTGAATTAATGGGAGTAAACACTTCAAAATTTCA 3044
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RESULT 3
 US-09-825-147-3
 ; Sequence 3, Application US/09825147
 ; Patent No. US20020042505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Yi
 ; APPLICANT: Kieke, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.
 ; APPLICANT: Friedlich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US20020042505A1 Human Ion Channel Protein and
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0160-USA
 ; CURRENT APPLICATION NUMBER: US/09/825,147
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 3111
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-825-147-3

Query Match 94.1%; Score 2890.8; DB 9; Length 3111;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY 1 GGGAGCGGCGATGAAGATGTGGAGTCGGGCGGCGGCGAGGTCGCTGAACTCGGAGCC 60
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 QY 121 GGTGGGCTGAGGAGAGCGCGCGGCGGCGAGGCGGCGGCGGCGAGGTCGCTGCTGGGCGGAG 180
 DB 276 GGTGGGCTGAGGAGAGCGCGCGGCGGCGAGGCGGCGGCGGCGAGGTCGCTGCTGGGCGGAG 335
 QY 181 CGGCTCTCTTACACGAGTACCGAGCTGCGGCGGCGAGGTCGCTGCTGGGCGGAG 240
 DB 336 CGGCTCTCTTACACGAGTACCGAGCTGCGGCGGCGAGGTCGCTGCTGGGCGGAG 395
 QY 241 AACTACCTGTACAGCGTGTGAGAGAGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 396 AACTACCTGTACAGCGTGTGAGAGAGCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
 QY 301 GTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 456 GTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 515
 QY 361 ACAAATTTGGCTTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 516 ACAAATTTGGCTTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
 QY 421 TTGAGGTCATCATTTGGAATCTGCTGCGGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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 QY 481 GGAAGACTGAGGTTTGTCTGAAAAGCCCTTCTGTGTATAGATACCAATGTTCTTATCGCT 540
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 DB 696 TCAATAGCAATGTTTCTGCAAAAACCTCAGAGGTAATATTTTTCACAGCTTGCATCAGA 755

QY 601 AGCTCCGTTTCCCTACAGATCCCTCGCATGTGTCGCGATGAGACCGAAGGGGAGGCACTTGG 660
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 DB 876 GGAATTTTGGTCTTATATTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
 QY 781 AAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 936 AAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995
 QY 841 GGTATGAGACAAAATCCCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 996 GGTATGAGACAAAATCCCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
 QY 901 CTCTTGGCATTTCTTTCTTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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 DB 1389 ACAGCCGAGGAGAGTCCCAACAAAGTCAGAAAGTGTGAGGCTTCAACCAAGCAACCGAGC 1448
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Db 1869 GTACAGTCCATTAATCCAAAGTGGATGCTGCTAAGACATCTATATCAAGGCTCTTGG 1928
Qy 1801 AAAGGCTGCTGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1929 AAAGGCTGCTGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1988
Qy 1861 CAGACATCTGACATCTAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1989 CAGACATCTGACATCTAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2048
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Db 2049 AGTGGCTGCTTATCCAGATCAATAGTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCT 2108
Qy 1981 AGCCCAATAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
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Db 2169 GCAACACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2228
Qy 2101 GCMAACCAATTAATACGACACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2229 GCMAACCAATTAATACGACACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2288
Qy 2161 CCTCTCCAGCCATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2289 CCTCTCCAGCCATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2348
Qy 2221 TTACAGGAAGATTTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2349 TTACAGGAAGATTTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2408
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Db 2409 GTTGCACTCAATCTCAACAGGACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2468
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Db 2529 CAAAACCTGATCAGTCCGACCGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2588
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Db 2589 GGCTCCAGAGGACCGCAATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2648
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Db 2709 GCCAGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2768
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RESULT 4
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803, 268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 94.1%; Score 2890.8; DB 19; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

Qy 1 GGCAGCGGATGAAGATGTGAGTGGGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 156 GGCAGCGGATGAAGATGTGAGTGGGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215
Qy 61 GGCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 216 GGCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275
Qy 121 GGTGGCTGAGGAGAGCGCGCGGAGGCAAGCAGGAGGCGCGGATGAGGCTGCTGCTGCTG 180
Db 276 GGTGGCTGAGGAGAGCGCGCGGAGGCAAGCAGGAGGCGCGGATGAGGCTGCTGCTGCTG 335
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Db 336 CCGCTCTTACAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 395
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Db 396 AACTACCTGTACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
Qy 301 GTTTTCTCTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Qy 361 ACAAATTTGCGCTCAAGTGGCTCTTGAATCTGAGTTCGTGATGTTGCTGCTTGGT 420
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QY 2581 GCCAGGAAAGCTGCTTTGATCAGACTCTTAAGACTGGAAGTCAAGATCATCTCAG 2640
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Db 2769 AGATTTGTAAAGCAGAGAAAGTACAGATGCCCTCAGCTTCAATGTCAAACTGAAA 2828
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RESULT 5
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1

; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-148-1

Query Match 93.0%; Score 2857.4; DB 9; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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1526 TTCCGGCCCTCGCTGCCCCCTCAAAAGTTCTCAGCCAAAACCATGATAGTCTGACACA 1585
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1681 GAACATGAGACCAACACACATCTCAGTATGCTGGGTGGTCAAGGTTGAAAAACAG 1740
1886 GAACATGAGACCAACACACATCTCAGTATGCTGGGTGGTCAAGGTTGAAAAACAG 1945
1741 GTACAGTCCATAGATTCAGATGAGATGAGCTGCTACTAGACATCTATCAACAGCTCTTCGG 1800
1946 GTACAGTCCATAGATTCAGATGAGATGAGCTGCTACTAGACATCTATCAACAGCTCTTCGG 2005
1801 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGATTCACACCTTTTGAATGAA 1860
2006 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGATTCACACCTTTTGAATGAA 2065
1861 CAGACATCTGACATCAAAAGCCCTGAGATAGCAAAAGATTTTCCGAGTTCCGACAAAAC 1920
2066 CAGACATCTGACATCAAAAGCCCTGAGATAGCAAAAGATTTTCCGAGTTCCGACAAAAC 2125
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2126 AGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCGAAGGCTCGACGTTCAATTCG 2185
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2101 GCAACCAATAATAATACGGAACCAAGCCAGCCCAACCACTTAACAGATCCCACT 2160
2306 GCAACCAATAATAATACGGAACCAAGCCAGCCCAACCACTTAACAGATCCCACT 2365
2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGACCCCTAACCTTCGAGGC 2220
2366 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGACCCCTAACCTTCGAGGC 2425
2221 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCCTCAAGAAATTTTCAG 2280
2426 TTACAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCCTCAAGAAATTTTCAG 2485
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2341 GAAACTCTGTTGTTCTGTCTGCTCCATGCTGCGAAGCACTTGGGCAATCTTTGCTGTG 2400

2546 GAAACTCTGTTGTTCTGTCTGTCTGCCATGTGCGGAAGCATTTGGGCAATCTTTGTCTGTG 2605
2401 CAAACCTGATCAGGTCGACCCGAGAACTGATATACAACTTTCAAGAGTGTAGTCAAGT 2460
2606 CAAACCTGATCAGGTCGACCCGAGAACTGATATACAACTTTCAAGAGTGTAGTCAAGT 2665
2461 GGCTCCAGAGGCGCCCAAGATTTTTCACCCCAATGGAAGGAATCCAAATGTTTATTAAGT 2520
2666 GGCTCCAGAGGCGCCCAAGATTTTTCACCCCAATGGAAGGAATCCAAATGTTTATTAAGT 2725
2521 GATGAAGAGTGGGTCCGGAAGACAGACAGACACTTTTATGATGCGCAGCCGACCT 2580
2726 GATGAAGAGTGGGTCCGGAAGACAGACAGACACTTTTATGATGCGCAGCCGACCT 2785
2581 GCCAGGAAAGCTGCTTTTGCATCAGCTCTCTTAAGACCTGGAAGGTCAAGATATCTCAG 2640
2786 GCCAGGAAAGCTGCTTTTGCATCAGCTCTCTTAAGACCTGGAAGGTCAAGATATCTCAG 2845
2641 AGCATTTGTAAAGCAGAGAAAGTACAGATGCGCTCAGCTGCTCATGTCAAACTGAAA 2700
2846 AGCATTTGTAAAGCAGAGAAAGTACAGATGCGCTCAGCTGCTCATGTCAAACTGAAA 2905
2701 TAAATCTTCATTTCTTTCAGGACATGACAGTTCTTTAGCCATACATATTCATGATGA 2760
2906 TAAATCTTCATTTCTTTCAGGACATGACAGTTCTTTAGCCATACATATTCATGATGA 2965
2761 ACTATTTCCAAAGCCCTTTTAAAGTTGAATTTGCAAAATTCGGAAAGATGAAAAG 2820
2966 ACTATTTCCAAAGCCCTTTTAAAGTTGAATTTGCAAAATTCGGAAAGATGAAAAG 3025
2821 CAGTTATTAAGCCCGTTACCTTTAATTCATGATAAATGATGTTAAG 2869
3026 CAGTTATTAAGCCCGTTACCTTTAATTCATGATAAATGATGTTAAG 3074

RESULT 6
US-10-399-489A-5
; Sequence 5, Application US/10399489A
; Publication No. US20050101004A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: ARGENTIERI, Thomas M.
; APPLICANT: SHELDON, Jeffrey H.
; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
; FILE REFERENCE: AM100620
; CURRENT APPLICATION NUMBER: US/10/399,489A
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/241,078
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/32371
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/281,428
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-489A-5

Query Match 93.0%; Score 2857.4; DB 21; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

1 GGCAGCGGATGAGAGATGTGAGTCCGCGCGGAGCGGCTGCTGAACTCGGACGCG 60
206 GGCAGCGGATGAGAGATGTGAGTCCGCGCGGAGCGGCTGCTGAACTCGGACGCG 265
61 GGCAGCGGAGCGGCTGCTGATCTGCTGGGACCCGCGGCGGACGCTTGTGTGGCGGCG 120
266 GGCAGCGGAGCGGCTGCTGATCTGCTGGGACCCGCGGCGGACGCTTGTGTGGCGGCG 325

QY 121 GGTGGCTTGAAGGAGACCGCCCGGAGCAAGCAAGGGGCCCGATGAGCTGTGGGAAAG 180
Db 326 GGTGGCTTGAAGGAGACCGCCCGGAGCAAGCAAGGGGCCCGATGAGCTGTGGGAAAG 385
QY 181 CCGCTCTTTTACACGAGTACCGAGAGCTGCGGCGCAAGCTCAAGTACCGGCGGATGCAAG 240
Db 386 CGCTCTCTTTACACGAGTACCGAGAGCTGCGGCGCAAGCTCAAGTACCGGCGGATGCAAG 445
QY 241 AACTACCTGTACACGAGTGTGAGAGACCCGCGGCTGGGCGCTTCACTTACCAAGCTTTC 300
Db 446 AACTACCTGTACACGAGTGTGAGAGACCCGCGGCTGGGCGCTTCACTTACCAAGCTTTC 505
QY 301 GTTTTCTCTCTGTCTTTGGTGTCTTGAATTTGTACAGTGTTCATCAATCCCTGAGCAC 360
Db 506 GTTTTCTCTCTGTCTTTGGTGTCTTGAATTTGTACAGTGTTCATCAATCCCTGAGCAC 565
QY 361 ACAAAATGGCCCTCAAGTGGCCCTTGAATCCCTGAGAGTGTGATGATTTGTGCTTTGGT 420
Db 566 ACAAAATGGCCCTCAAGTGGCCCTTGAATCCCTGAGAGTGTGATGATTTGTGCTTTGGT 625
QY 421 TTGGAATTCATCATTCGAAATCTGTCTGGGAGTGTGCTTTGTGATATAGAGATGGCAA 480
Db 626 TTGGAATTCATCATTCGAAATCTGTCTGGGAGTGTGCTTTGTGATATAGAGATGGCAA 685
QY 481 GGAAGACTGAGGTTTCTCGAAAACCCCTTCTGTGTATAGATACATTTGCTTATCGCT 540
Db 686 GGAAGACTGAGGTTTCTCGAAAACCCCTTCTGTGTATAGATACATTTGCTTATCGCT 745
QY 541 TCAATGACGTTGTTCTGCAAAACCTCAAGGGTATATTTTGGCCAGCTGACACTGACA 600
Db 746 TCAATGACGTTGTTCTGCAAAACCTCAAGGGTATATTTTGGCCAGCTGACACTGACA 805
QY 601 AGTCTCCGTTTCTCTACAGATCTCTCCGATGTGCGGATGAGACCGAGGGAGCACTTGG 660
Db 806 AGTCTCCGTTTCTCTACAGATCTCTCCGATGTGCGGATGAGACCGAGGGAGCACTTGG 865
QY 661 AAATTACTGGGTTCAAGTGTATATGCTCAACAGCAAGAAATTAATCAAGCTTGTATATA 720
Db 866 AAATTACTGGGTTCAAGTGTATATGCTCAACAGCAAGAAATTAATCAAGCTTGTATATA 925
QY 721 GGATTTTGGTCTTATTTTTCGTTCTTCTGTCTATCTGGTGAAGAAAGATGCAAT 780
Db 926 GGATTTTGGTCTTATTTTTCGTTCTTCTGTCTATCTGGTGAAGAAAGATGCAAT 985
QY 781 AAAGATTTTCTACATATGAGATGCTCTGTGTGGGCACAATTAATTAATTAATTAAT 840
Db 986 AAAGATTTTCTACATATGAGATGCTCTGTGTGGGCACAATTAATTAATTAATTAAT 1045
QY 841 GGCTATGAGACAAAACCTCCCTTAATTTGGCTGGGAAGATTGCTTCTGCAAGCTTTGCA 900
Db 1046 GGCTATGAGACAAAACCTCCCTTAATTTGGCTGGGAAGATTGCTTCTGCAAGCTTTGCA 1105
QY 901 CTCTCTGGGATTTCTTTCTTTGCACTTCTGCGCGGCAATCTTGGGCTCAGGTTTGGATTA 960
Db 1106 CTCTCTGGGATTTCTTTCTTTGCACTTCTGCGCGGCAATCTTGGGCTCAGGTTTGGATTA 1165
QY 961 AAAGTACAAAGAACAAACACCGCCAGAAACATTTGAGAAAAAGAAAGAACCCAGCTGCAAC 1020
Db 1166 AAAGTACAAAGAACAAACACCGCCAGAAACATTTGAGAAAAAGAAAGAACCCAGCTGCAAC 1225
QY 1021 CTCATTTCAAGTGTGTGTGGGCTTATAGCAAGCTGATGAGAAATCTGTTTCAATGGCAAC 1080
Db 1226 CTCATTTCAAGTGTGTGTGGGCTTATAGCAAGCTGATGAGAAATCTGTTTCAATGGCAAC 1285
QY 1081 TGAAGCCCACTTGAAGGCTTGAACACCTGACCTTACCAAGAAAGAAACAAAGGGGAA 1140
Db 1286 TGAAGCCCACTTGAAGGCTTGAACACCTGACCTTACCAAGAAAGAAACAAAGGGGAA 1345
QY 1141 GCATCAAGCAGTCAAGAGTAAAGTTTAAAGACGAGTGCATGGCTAAGCCCAAGGGGC 1200
Db 1346 GCATCAAGCAGTCAAGAGTAAAGTTTAAAGACGAGTGCATGGCTAAGCCCAAGGGGC 1405
QY 1201 CAGAGTATTAAGAGCCGACAAAGCTCAAGTAAAGTGAAGAGGTCCCAAGCACCGACATC 1260

Db 1406 CAGAGTATTAAGAGCCGACAAAGCTCAGTAAAGTGAAGAGGTCCCAAGCACCGACATC 1465
QY 1261 ACAGCCGAGGAGAGTCCCAACCAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
Db 1466 ACAGCCGAGGAGAGTCCCAACCAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1525
QY 1321 TTCCGGCCCTGCTGCGCTCAAAAGTTCTGAGCCCAACAGTATGATAGTGTACACA 1380
Db 1526 TTCCGGCCCTGCTGCGCTCAAAAGTTCTGAGCCCAACAGTATGATAGTGTACACA 1585
QY 1381 GCCCTTGGCATGATGATGATATGATGATAAAAGATGCCAGTGTGATGATCACTGGAA 1440
Db 1586 GCCCTTGGCATGATGATGATATGATGATAAAAGATGCCAGTGTGATGATCACTGGAA 1645
QY 1441 GACCTCACCCCAACGCTTAAACGTCATTTGAGCTATCAGAAATTAATAATTCATGAT 1500
Db 1646 GACCTCACCCCAACGCTTAAACGTCATTTGAGCTATCAGAAATTAATAATTCATGAT 1705
QY 1501 GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAGATGTCAATTGAACA 1560
Db 1706 GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAGATGTCAATTGAACA 1765
QY 1561 TATTCTGCTGGTCACTGGAACATGTTGTGTAATTAAGCTTCAAAACAGCTTGTAT 1620
Db 1766 TATTCTGCTGGTCACTGGAACATGTTGTGTAATTAAGCTTCAAAACAGCTTGTAT 1825
QY 1621 CAAATTTCTGGAAAAGGGCAATCAATCAGATTAAGAGCCGAGAGAAATTAACAGA 1680
Db 1826 CAAATTTCTGGAAAAGGGCAATCAATCAGATTAAGAGCCGAGAGAAATTAACAGA 1885
QY 1681 GAACATGAGACCAACAGATCTCAGATGCTCGGTGCGGTGCTCAAGTTGAAAGAAACAG 1740
Db 1886 GAACATGAGACCAACAGATCTCAGATGCTCGGTGCGGTGCTCAAGTTGAAAGAAACAG 1945
QY 1741 GTACAGTCAATAGAAATCCAGCTGAGCTGCTTACAGCATCTATCAACAGTCTTGG 1800
Db 1946 GTACAGTCAATAGAAATCCAGCTGAGCTGCTTACAGCATCTATCAACAGTCTTGG 2005
QY 1801 AAAGGCTCTGAGCTGAGCCCTGCTTGGCTTCAATCCAGTCCCACTTTGAAATGTGA 1860
Db 2006 AAAGGCTCTGAGCTGAGCCCTGCTTGGCTTCAATCCAGTCCCACTTTGAAATGTGA 2065
QY 1861 CAGACATCTGATCAATCAAGCCCTGTGTGATAGCAAAAGATCTTTCGGTTCGCAAAAAC 1920
Db 2066 CAGACATCTGATCAATCAAGCCCTGTGTGATAGCAAAAGATCTTTCGGTTCGCAAAAAC 2125
QY 1921 AGTGGCTGCTTATCCAGATCAATAGTGCCAACATCTGAGAGGCTTGCAGTTCATTCG 1980
Db 2126 AGTGGCTGCTTATCCAGATCAATAGTGCCAACATCTGAGAGGCTTGCAGTTCATTCG 2185
QY 1981 ACGCAATAGAGTTCAAGTGCACAGCTTCTACGCGCTTACCCCTACATGACAGTCAA 2040
Db 2186 ACGCAATAGAGTTCAAGTGCACAGCTTCTACGCGCTTACCCCTACATGACAGTCAA 2245
QY 2041 GCAACACAGGTGCCAATTAATCAAGCGATGCTCAGCAGTGGACCCACCAACCAAT 2100
Db 2246 GCAACACAGGTGCCAATTAATCAAGCGATGCTCAGCAGTGGACCCACCAACCAAT 2305
QY 2101 GCAAAACCAATTAATTAAGGACCCCAAGCAGAGCCCAACCAATTAATTAATTAATTAAT 2160
Db 2306 GCAAAACCAATTAATTAAGGACCCCAAGCAGAGCCCAACCAATTAATTAATTAATTAAT 2365
QY 2161 CCTCTCCAGGCATCAAGCATCTGCCGAGGCAAGAACTGTGCAACCTTACCTGCAAGC 2220
Db 2366 CCTCTCCAGGCATCAAGCATCTGCCGAGGCAAGAACTGTGCAACCTTACCTGCAAGC 2425
QY 2221 TTACAGAAAGCAATTTTGAAGTCAACACCTGCTTGTGCTTCAAGAAATTTGTCAG 2280
Db 2426 TTACAGAAAGCAATTTTGAAGTCAACACCTGCTTGTGCTTCAAGAAATTTGTCAG 2485
QY 2281 GTTGCACAGTCAATTTCAACCAAGACCGTTCTATGAGAAAGCTTTGAACATGGGAAGA 2340

Db 2486 GTTGCACAGTCMAATCTCACCAAGACCGCTTATGAGAAAGCTTTGACATGGAGGA 2545
Qy 2341 GAAACTGTGTGTCTGTCTGTCCATGATGCGCAAGAACTTGGCAAACTTTGTCTGTG 2400
Db 2546 GAAACTGTGTGTCTGTCTGTCCATGATGCGCAAGAACTTGGCAAACTTTGTCTGTG 2605
Qy 2401 CAAAACCTGATCAGTGTGACCGAGAACTGAAATATACAACTTTGAGGATGATCAAGT 2460
Db 2606 CAAAACCTGATCAGTGTGACCGAGAACTGAAATATACAACTTTGAGGATGATCAAGT 2665
Qy 2461 GGGTCCAGAGAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTA 2520
Db 2666 GGGTCCAGAGAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTA 2725
Qy 2521 GATGAAGAGGTGGGTCCCGAAGAGACAGAGACACACTTTGATGCGGACCGCAAGCT 2580
Db 2726 GATGAAGAGGTGGGTCCCGAAGAGACAGAGACACACTTTGATGCGGACCGCAAGCT 2785
Qy 2581 GCCAGGGAAGCTCCCTTTCATCAGACTCTCTAAGACTGGAAGTCAAGATCATCTCAG 2640
Db 2786 GCCAGGGAAGCTCCCTTTCATCAGACTCTCTAAGACTGGAAGTCAAGATCATCTCAG 2845
Qy 2641 AGCATTTGTAAGGACAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
Db 2846 AGCATTTGTAAGGACAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2905
Qy 2701 TAAGTCTTCATTTCTTTCAGGCAATAGCAGTTCTTAGCAATATCATTTGATGA 2760
Db 2906 TAAGTCTTCATTTCTTTCAGGCAATAGCAGTTCTTAGCAATATCATTTGATGA 2965
Qy 2761 ACTATTTGCAAAAGCCCTTCTMAAAGTTGCAAAATGCGGAGAACTGAAAAG 2820
Db 2966 ACTATTTGCAAAAGCCCTTCTMAAAGTTGCAAAATGCGGAGAACTGAAAAG 3025
Qy 2821 CAGTTATTAAGCCCGTTACTTTTAATGTCATGAAAATGATGTTTAAAG 2869
Db 3026 CAGTTATTAAGCCCGTTACTTTTAATGTCATGAAAATGATGTTTAAAG 3074

RESULT 7
US-10-482-834A-55
; Sequence 55, Application US/10482834A
; Publication No.: US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hilary Ann
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Biomimics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 55
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-55

Query Match 93.0%; Score 2855.8; DB 21; Length 3074;
Best Local Similarity 99.7%; Pired. No. 0;
Matches 2860; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGCAGCGGATGAAGATGTGAGTGGCGCGCGGAGAGGTGTGCTGAATCTGGACGCC 60
Db 206 GGCAGCGGATGAAGATGTGAGTGGCGCGCGGAGAGGTGTGCTGAATCTGGACGCC 265

Qy 61 GCCAGGGGCGACGGCGCTGCTACTGCTGGGCAACCGCGGGCCACGCTTGTGGCGGCGC 120
Db 266 GCCAGGGGCGACGGCGCTGCTACTGCTGGGCAACCGCGGGCCACGCTTGTGGCGGCGC 325
Qy 121 GGTGGCTTGAAGGAGAGCGCGCGGGCAAGCAGAGGGGCGCGGATGAGCCTGTGGGAAAG 180
Db 326 GGTGGCTTGAAGGAGAGCGCGCGGGCAAGCAGAGGGGCGCGGATGAGCCTGTGGGAAAG 385
Qy 181 CCGCTCTTAAACGAGTATGCGCAAGCTCCCGGCGCAAGTCAAGTACCGGCGGGTGCAG 240
Db 386 CCGCTCTTAAACGAGTATGCGCAAGCTCCCGGCGCAAGTCAAGTACCGGCGGGTGCAG 445
Qy 241 AACTACTGTATCAACGCTGTGAGAGACCCCGGCGCTGGGCGTTCACTACACGCTTTC 300
Db 446 AACTACTGTATCAACGCTGTGAGAGACCCCGGCGCTGGGCGTTCACTACACGCTTTC 505
Qy 301 GTTTTCTCCTTGTCTTGTGGTGTGATTTGTGCAAGTGTTCATCCATCCCTGAGCAC 360
Db 506 GTTTTCTCCTTGTCTTGTGGTGTGATTTGTGCAAGTGTTCATCCATCCCTGAGCAC 565
Qy 361 ACAAAATTTGGCCCAAGTTGCCCTTGTATCCTGAGATTTGTATGATGATTTGTGCTTGGT 420
Db 566 ACAAAATTTGGCCCAAGTTGCCCTTGTATCCTGAGATTTGTATGATGATTTGTGCTTGGT 625
Qy 421 TTGAGATTCATGATTCGAATCTGTCTGCGGGTGTGCTGTGATATAGAGATGGCAA 480
Db 626 TTGAGATTCATGATTCGAATCTGTCTGCGGGTGTGCTGTGATATAGAGATGGCAA 685
Qy 481 GGAAGACTGAGGTTTGTCTGAAAAGCCCTTCTGTGTATAGATACATTTCTTATGCGCT 540
Db 686 GGAAGACTGAGGTTTGTCTGAAAAGCCCTTCTGTGTATAGATACATTTCTTATGCGCT 745
Qy 541 TCAATTCGAGTTGTTCTTCCGCAAAAACCTCAGGGTAATTTTGGCCGCTGCTGACAC 600
Db 746 TCAATTCGAGTTGTTCTTCCGCAAAAACCTCAGGGTAATTTTGGCCGCTGCTGACAC 805
Qy 601 AGTCTCCGTTTCTTACAGATCTCTCGCATGTGCGCATGAGACGGAAGGAGCACTTGG 660
Db 806 AGTCTCCGTTTCTTACAGATCTCTCTCGCATGTGCGCATGAGACGGAAGGAGCACTTGG 865
Qy 661 AAATTACTGGGTTCAAGTGTGTTATGCTCAACAGAAATTAATCAACGCTTGTGATATA 720
Db 866 AAATTACTGGGTTCAAGTGTGTTATGCTCAACAGAAATTAATCAACGCTTGTGATATA 925
Qy 721 GGAATTTGGTCTTAATTTTTCGCTTCCCTTGTCTATCTGTGGAAGAAAGATGCCAAT 780
Db 926 GGAATTTGGTCTTAATTTTTCGCTTCCCTTGTCTATCTGTGGAAGAAAGATGCCAAT 985
Qy 781 AAAGAGTTTCTACATATGCAATGCTCTGTGTGGGCAACAATTACATTGACCACTATT 840
Db 986 AAAGAGTTTCTACATATGCAATGCTCTGTGTGGGCAACAATTACATTGACCACTATT 1045
Qy 841 GGCATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTTGCTTTCAGGCTTTTGA 900
Db 1046 GGCATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTTGCTTTCAGGCTTTTGA 1105
Qy 901 CTCCTTGGATTTCTTCTTTCGACATCTCTGCGGCAATCTTGGCTCAGGTTTGCATTA 960
Db 1106 CTCCTTGGATTTCTTCTTTCGACATCTCTGCGGCAATCTTGGCTCAGGTTTGCATTA 1165
Qy 961 AAAGTACAAAGAACACCGCGCAGAAACACTTTGAGAAAGAAAGAAACCCAGCTGCAAC 1020
Db 1166 AAAGTACAAAGAACACCGCGCAGAAACACTTTGAGAAAGAAAGAAACCCAGCTGCAAC 1225
Qy 1021 CTCATTCAGTGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTTCAATTCACACC 1080
Db 1226 CTCATTCAGTGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTTCAATTCACACC 1285
Qy 1081 TGGAGGCCACACTTGAAGGCTTTGACACCTTCACACCCCTACCAAAAGAAACAAAGGGAA 1140
Db 1286 TGGAGGCCACACTTGAAGGCTTTGACACCTTCACACCCCTACCAAAAGAAACAAAGGGAA 1345
Qy 1141 GCATCAAGCAGTCAGAAAGTTTAAAGAGCAGTGGCATGGCTAGCCCGAGGGGC 1200

1346 GCATCAAGCAGTCAGAAAGTTTAAAGAGCAGTGGCGATGGCTAGCCCGACAGGGGC 1405
1201 CAGAGATTAAAGCCGCGACAAAGCTCAGTAGTGAAGAGGTCGCCAAGCACCCGACATC 1260
1406 CAGAGATTAAAGCCGCGACAAAGCTCAGTAGTGAAGAGGTCGCCAAGCACCCGACATC 1465
1261 ACAGCCGAGGGCAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGC 1320
1466 ACAGCCGAGGGCAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGC 1525
1321 TTCGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAAACAGTGAATGATGCTGACACA 1380
1526 TTCGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAAACAGTGAATGATGCTGACACA 1585
1381 GCCCTTGGCAGTGAATGATATGATGAAGAAAGTGCAGAGTGAATGATCAGTGAAGAA 1440
1586 GCCCTTGGCAGTGAATGATATGATGAAGAAAGTGCAGAGTGAATGATCAGTGAAGAA 1645
1441 GACCTCAGCCCGACCACTTAAACTGTCAATTCAGCTATGAGAAATTAAGAAATTTTCATGTT 1500
1646 GACCTCAGCCCGACCACTTAAACTGTCAATTCAGCTATGAGAAATTAAGAAATTTTCATGTT 1705
1501 GCAAAACGGAAGTTTAAAGAAACCTTAAGTCCATATGATGTAAGAAAGATGATCATTTGAACA 1560
1706 GCAAAACGGAAGTTTAAAGAAACCTTAAGTCCATATGATGTAAGAAAGATGATCATTTGAACA 1765
1561 TATTCGCTGGTCAATCGGACATGTTGTGATGAATTAAGAAACCTTAAACAGCTGTGAT 1620
1766 TATTCGCTGGTCAATCGGACATGTTGTGATGAATTAAGAAACCTTAAACAGCTGTGAT 1825
1621 CAAATTCCTTGAAGAAAGGCAAAATCAGATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1680
1826 CAAATTCCTTGAAGAAAGGCAAAATCAGATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1885
1681 GAACATGAAGACCAAGACGATCTCAGTATGCTCGGTGGGTCAAGSTTGAAGAAACAG 1740
1886 GAACATGAAGACCAAGACGATCTCAGTATGCTCGGTGGGTCAAGSTTGAAGAAACAG 1945
1741 GTACAGTCCATAGATTCAGAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTCCG 1800
1946 GTACAGTCCATAGATTCAGAGCTGAGCTGCTTCTAGACATCTATCAACAGGCTCTTCCG 2005
1801 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGTTCACGTTCCACCTTTGAATGAA 1860
2006 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGTTCACGTTCCACCTTTGAATGAA 2065
1861 CAGACATCTGACATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCCGACAAAAC 1920
2066 CAGACATCTGACATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCCGACAAAAC 2125
1921 AGTGGCTGCTTACAGATCAACTAGTGCACATCTCGAGAGGCTGAGGATTCATTTG 1980
2126 AGTGGCTGCTTACAGATCAACTAGTGCACATCTCGAGAGGCTGAGGATTCATTTG 2185
1981 AGCCCAAAATGAGTTGAGTCCGACCACTTTCTACGCGCTTAGCCCTTATGACAGTCAA 2040
2186 AGCCCAAAATGAGTTGAGTCCGACCACTTTCTACGCGCTTAGCCCTTATGACAGTCAA 2245
2041 GGAACACAGTGGCAATTAAGTCAAAAGCGATGGTCAAGCTGAGACCCCAACACCAAT 2100
2246 GGAACACAGTGGCAATTAAGTCAAAAGCGATGGTCAAGCTGAGACCCCAACACCAAT 2305
2101 GGAACACCAATTAATACGCAACCAAGCAGACGACCCCAACCACTTTAAGATCCCACT 2160
2306 GGAACACCAATTAATACGCAACCAAGCAGACGACCCCAACCACTTTAAGATCCCACT 2365
2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCGAAGAACTCTGACCCCTAACCTTCAGGCG 2220
2366 CCTCTCCAGCCATCAAGCATCTGCCAGGCGAAGAACTCTGACCCCTAACCTTCAGGCG 2425
2221 TTACAGAAAGCATTTCTGACGTCACCACTGCTTGTGCTTCCAAAGAAATGTTTCG 2280

2426 TTACAGAAAGCATTTCTGACGTCACCACTGCTTGTGCTCCAGAGAAATGTTTCG 2485
2281 GTTGACAGTCAAAATCTCACCAAGGACCGTTCTATGAGAGAAAGCTTTGACATGGAGGA 2340
2486 GTTGACAGTCAAAATCTCACCAAGGACCGTTCTATGAGAGAAAGCTTTGACATGGAGGA 2545
2341 GAAACTGTGTCTGTCTGTCTGTCACAGTGTGCGAAGGACTTGGGCAAACTTTGTCTGTG 2400
2546 GAAACTGTGTCTGTCTGTCTGTCACAGTGTGCGAAGGACTTGGGCAAACTTTGTCTGTG 2605
2401 CAAAACCTGATCAGTCCAGCAGAGAACTGAATATACAACTTTACAGGAGTGAATCAAGT 2460
2606 CAAAACCTGATCAGTCCAGCAGAGAACTGAATATACAACTTTACAGGAGTGAATCAAGT 2665
2461 GAGCTCCAGAGGCGACAGATTTTAACTCCCAATGAGAGGAAATCCAAATGTTTAACT 2520
2666 GAGCTCCAGAGGCGACAGATTTTAACTCCCAATGAGAGGAAATCCAAATGTTTAACT 2725
2521 GATGAAGAGTGGTGTCCGAAAGACAGAGACAGACACTTTTATGATGCGCACCGACCT 2580
2726 GATGAAGAGTGGTGTCCGAAAGACAGAGACAGACACTTTTATGATGCGCACCGACCT 2785
2581 GCGAGGGAAGCTGCTTTGATCAGACATCTCTTAAGACTGGAAGGTCAGATCATCTGAG 2640
2786 GCGAGGGAAGCTGCTTTGATCAGACATCTCTTAAGACTGGAAGGTCAGATCATCTGAG 2845
2641 AGCATTTGTAAGGCGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
2846 AGCATTTGTAAGGCGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2905
2701 TAACTTCTTCAATTTCTTTCCAGGCAATGACAGTCTTTAGCCATACATATCATGATGA 2760
2906 TAACTTCTTCAATTTCTTTCCAGGCAATGACAGTCTTTAGCCATACATATCATGATGA 2965
2761 ACTATTTGGAAGAGCCCTCTAAAAAGTGAATGCAAGATTCGGAGAAACATGAAAGG 2820
2966 ACTATTTGGAAGAGCCCTCTAAAAAGTGAATGCAAGATTCGGAGAAACATGAAAGG 3025
2821 CAGTTTATAGCCCGTTACTTTTATTTGATGAGAAATGCAATGTTTAGG 2869
3026 CAGTTTATAGCCCGTTACTTTTATTTGATGAGAAATGCAATGTTTAGG 3074

RESULT 8
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKORFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCMOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
10 ATGAAGATGTGAGTCCGGCCGGGGCAGGGTCTGTGAACTCGGACGCCCGCAGGGGC 69

Db	1	ATGAAAGATGTGTGAATCGGGGCGGGGGGCAAGGGTGTCTGTGAATCTGGCAAGCCGCAAGGGG	60
Qy	70	GACGGCTGTCTACTGTCTGGGCACCCGCGCGGCAAGCTTTGGTGGCGGCGGTGGCTGTG	129
Db	61	GACGGCTGTCTACTGTCTGGGCACCCGCGCGGCAAGCTTTGGTGGCGGCGGTGGCTGTG	120
Qy	130	AGGGAAGACCCCGCGGGGCAAGCAAGGGGGGCGGATGAAGCTGTCTGGGAAGCCGTCTCT	189
Db	121	AGGGAAGACCCCGCGGGGCAAGCAAGGGGGGCGGATGAAGCTGTCTGGGAAGCCGTCTCT	180
Qy	190	TACACGAGTACGACAGGCTGCCCGGCGCAACGTCAAGTACCGGGGGGTACAACTACCTG	249
Db	181	TACACGAGTACGACAGGCTGCCCGGCGCAACGTCAAGTACCGGGGGGTACAACTACCTG	240
Qy	250	TACAAAGTGTGAGAGAGACCCCGCGCGGTGGCGTTCACTCAACAGCTTTGGTTTTCTC	309
Db	241	TACAAAGTGTGAGAGAGACCCCGCGCGGTGGCGTTCACTCAACAGCTTTGGTTTTCTC	300
Qy	310	CTTGTCTTTGGTGTCTGATATTTTGTCAAGTTTTTCTACATTCCTTGAGACACAATAATG	369
Db	301	CTTGTCTTTGGTGTCTGATATTTTGTCAAGTTTTTCTACATTCCTTGAGACACAATAATG	360
Qy	370	GCCCTAAATGGCTCTTGAATCTCTGAGTTGCGAGTTCGAGATTTGCTTTGGTTGGAGTTC	429
Db	361	GCCCTAAATGGCTCTTGAATCTCTGAGTTGCGAGTTCGAGATTTGCTTTGGTTGGAGTTC	420
Qy	430	ATCATTCGAATCTGGTCTGCGGGTGTCTGTTGTGCACTATTAAGATGTGCAAGAAAGCTG	489
Db	421	ATCATTCGAATCTGGTCTGCGGGTGTCTGTTGTGCACTATTAAGATGTGCAAGAAAGCTG	480
Qy	490	AGGTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTATGCTTCAATAGCA	549
Db	481	AGGTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTATGCTTCAATAGCA	540
Qy	550	GTTGTTTCTGAAAAAATCTCAGGGTAAATTTTGGCAAGTCTGCACTCAGAAGTCTCGGT	609
Db	541	GTTGTTTCTGAAAAAATCTCAGGGTAAATTTTGGCAAGTCTGCACTCAGAAGTCTCGGT	600
Qy	610	TTCTCAACAGATCTCTCCGATGGTGGGCAATGACCGAAGGGAGGCACTTGGAAATTAATCTG	669
Db	601	TTCTCAACAGATCTCTCCGATGGTGGGCAATGACCGAAGGGAGGCACTTGGAAATTAATCTG	660
Qy	670	GATTCAAGTGTATATGCTCACAAGCAAGAAATTAATCAAGCTTGGTACATAGATTTTGTG	729
Db	661	GATTCAAGTGTATATGCTCACAAGCAAGAAATTAATCAAGCTTGGTACATAGATTTTGTG	720
Qy	730	GTTCTTATATTTTGTGTCTTCTTGTCTATCTGGTGGAAAAAGATGCCAATAAAGATTT	789
Db	721	GTTCTTATATTTTGTGTCTTCTTGTCTATCTGGTGGAAAAAGATGCCAATAAAGATTT	780
Qy	790	TCTCATATGAGATGCTCTCGGTGGGGGCAATTAATTAATGACAACATTTGGGCTATGGA	849
Db	781	TCTCATATGAGATGCTCTCGGTGGGGGCAATTAATTAATGACAACATTTGGGCTATGGA	840
Qy	850	GACAAATCTCCCTACTTGTGCTGGGAAGATTTGTTCTGCAAGCTTTGCACTCTTGGC	909
Db	841	GACAAATCTCCCTACTTGTGCTGGGAAGATTTGTTCTGCAAGCTTTGCACTCTTGGC	900
Qy	910	ATTTCTTTCTTTGCACTTCTGCGCGGCAATCTTGGCTCAGGTTTTGCACTTAAAGTACAA	969
Db	901	ATTTCTTTCTTTGCACTTCTGCGCGGCAATCTTGGCTCAGGTTTTGCACTTAAAGTACAA	960
Qy	970	GACAAACCGGCAAGAAACATTTGAGAAAAAGAAAGAACCCAGGCTGCCAATCTATTCAG	1029
Db	961	GACAAACCGGCAAGAAACATTTGAGAAAAAGAAAGAACCCAGGCTGCCAATCTATTCAG	1020
Qy	1030	TGTGTTTGGCGTATGTTACGCAAGCTGATGAGAAATCTGTTTCCATTTGCAACTGTGAAGCA	1089
Db	1021	TGTGTTTGGCGTATGTTACGCAAGCTGATGAGAAATCTGTTTCCATTTGCAACTGTGAAGCA	1080
Qy	1090	CACTTGAAGGCTTGCACACTGCAAGCCCTTACCAAGAAAAACAAGGGAGATCAAGC	1149

Db	1081	CAC TTGAAGGCCTTGACACACCTGACGCCCTTACCAAGAAAAGAACAGGGAGACATCAGC	1140
Qy	1150	AGTCAGAAAGCTAAAGTTTAAAGAGCCAGTGCAGTGGCTTAAGCCCAAGGGCCAGAGTATT	1209
Db	1141	AGTCAGAAAGCTAAAGTTTAAAGAGCCAGTGCAGTGGCTTAAGCCCAAGGGCCAGAGTATT	1200
Qy	1210	AAGAGCCGACAGAGCTCAGTAGGTGACAGAGAGTCCCCAAGCACCGACATCAAGCCGAG	1269
Db	1201	AAGAGCCGACAGAGCTCAGTAGGTGACAGAGAGTCCCCAAGCACCGACATCAAGCCGAG	1260
Qy	1270	GGCAGTCCCAACAAAGTGCAGAAAGAGGTGGAGCTTACAGACCGAAGCCGGCTTCGGGGCC	1329
Db	1261	GGCAGTCCCAACAAAGTGCAGAAAGAGTGGAGCTTACAGACCGAAGCCGGCTTCGGGGCC	1320
Qy	1330	TCGCTGGCGCTCAAAAAGTTCTCAGCCAAAACCAAGTATGATGCTTGACACAGCCCTTGGC	1389
Db	1321	TCGCTGGCGCTCAAAAAGTTCTCAGCCAAAACCAAGTATGATGCTTGACACAGCCCTTGGC	1380
Qy	1390	ACTGATGATGATATGATGAAAAAGATGCGAGTGTGATGATCAGTGGAAAGCTCACC	1449
Db	1381	ACTGATGATGATATGATGAAAAAGATGCGAGTGTGATGATCAGTGGAAAGCTCACC	1440
Qy	1450	CCACACCTTAAACCTGTCATTCGAGGCTATCAGAAATTATGAAATTTTCATGTCGAAAAAGG	1509
Db	1441	CCACACCTTAAACCTGTCATTCGAGGCTATCAGAAATTATGAAATTTTCATGTCGAAAAAGG	1500
Qy	1510	AAGTTTAAAGGAAACRTTACGTCCTCATATGATGTAAAGATGTCATTTGAAACATATTTCTCT	1569
Db	1501	AAGTTTAAAGGAAACGTTACGTCCTCATATGATGTAAAGATGTCATTTGAAACATATTTCTCT	1560
Qy	1570	GGTCATCTGGACATGTTGTGTGATGATTTAAAGCCTTCAACACGTTGTATCAATTTCTT	1629
Db	1561	GGTCATCTGGACATGTTGTGTGATGATTTAAAGCCTTCAACACGTTGTATCAATTTCTT	1620
Qy	1630	GGAAAAGGGCAATTCATATCAGATTAAGAAAGCCGAGAGAAAATTAACACAGAACATGAG	1689
Db	1621	GGAAAAGGGCAATTCATATCAGATTAAGAAAGCCGAGAGAAAATTAACACAGAACATGAG	1680
Qy	1690	ACCACAGACGATCTCAGTATGCTCGGTGGGTGATCAGAGTTGTAAGAACAGTACAGTCC	1749
Db	1681	ACCACAGACGATCTCAGTATGCTCGGTGGGTGATCAGAGTTGTAAGAACAGTACAGTCC	1740
Qy	1750	ATAGAAATCCAGCTGAGCTGCCCTTACATGACATCTTATCAACAGTCTCTTGGAAAGCTCT	1809
Db	1741	ATAGAAATCCAGCTGAGCTGCCCTTACATGACATCTTATCAACAGTCTCTTGGAAAGCTCT	1800
Qy	1810	GCCTCACGCCCTCGCTTGGCTTATTCAGCTTCCAGCTTTTGAATGTGAACAGACATCT	1869
Db	1801	GCCTCACGCCCTCGCTTGGCTTATTCAGCTTCCAGCTTTTGAATGTGAACAGACATCT	1860
Qy	1870	GACTATCAAAAGCCCTGTGATGACAAAGATCTTTCGGGTTCGSCAACAAACAGTGGCTGC	1929
Db	1861	GACTATCAAAAGCCCTGTGATGACAAAGATCTTTCGGGTTCGSCAACAAACAGTGGCTGC	1920
Qy	1930	TTATTCAGATCAACTAGTGCACATCTCGAGAGGCTCAGTTCAATTTCGACGCCCAAT	1989
Db	1921	TTATTCAGATCAACTAGTGCACATCTCGAGAGGCTCAGTTCAATTTCGACGCCCAAT	1980
Qy	1990	GAGTTTCAGTGCACAGATCTTCTACGCGGCTTAAGCCCTTACTATGACACGTACAGCAACAG	2049
Db	1981	GAGTTTCAGTGCACAGATCTTCTACGCGGCTTAAGCCCTTACTATGACACGTACAGCAACAG	2040
Qy	2050	GTGCAATTAATGTCGAAAGCAGTGGCTCAGCAGTGGAGCCACCAACCAATTGCAACCA	2109
Db	2041	GTGCAATTAATGTCGAAAGCAGTGGCTCAGCAGTGGAGCCACCAACCAATTGCAACCA	2100
Qy	2110	ATAAATACGGCACCACCAAGCCAGCAGGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2169
Db	2101	ATAAATACGGCACCACCAAGCCAGCAGGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Qy	2170	GCCATCAAGCATCTGCCACGAGCCAGAAACTCTGTGACACCTTAACCTTCGAGGCTTAACAGAA	2229
Db	2161	GCCATCAAGCATCTGCCACGAGCCAGAAACTCTGTGACACCTTAACCTTCGAGGCTTAACAGAA	2220

QY 2230 AGCATTTCTGACGTCAACCACTGCTGTGTGCTCCAGAGAAATGTCAGGTTGCACAG 2289
DB 2221 AGCATTTCTGAGGTCAACCACTGCTGTGTGCTCCAGAGAAATGTCAGGTTGCACAG 2280
QY 2290 TCATATCTCAACCAAGACCGTTTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2349
DB 2281 TCATATCTCAACCAAGACCGTTTATAGAGAAAAGCTTTGACATGGAGAGAACTCTG 2340
QY 2350 TTGTCTGTCTGTCCATGGTGGCGAAGGACTTGGGAAATCTTGTCTGTGCAAAACCTG 2409
DB 2341 TTGTCTGTCTGTCCATGGTGGCGAAGGACTTGGGAAATCTTGTCTGTGCAAAACCTG 2400
QY 2410 ATCAGGTGACCGAGAACTGAATATACAACTTTGAGGAGTGAATCAAGTGGCTTCAGA 2469
DB 2401 ATCAGGTGACCGAGAACTGAATATACAACTTTGAGGAGTGAATCAAGTGGCTTCAGA 2460
QY 2470 GGCAGCCAGATTTTATACCCAAATGAGAGGAATCCAAATTTTATTAATGATGAAG 2529
DB 2461 GGCAGCCAGATTTTATACCCAAATGAGAGGAATCCAAATTTTATTAATGATGAAG 2520
QY 2530 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGGACCGAGGCTGCAAGGAA 2589
DB 2521 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGGACCGAGGCTGCAAGGAA 2580
QY 2590 GCTGCTTTGATCAGACTCTCTTAAGGACTGAAAGTCAAGATCATCTGAGGATTTGT 2649
DB 2581 GCTGCTTTGATCAGACTCTCTTAAGGACTGAAAGTCAAGATCATCTGAGGATTTGT 2640
QY 2650 AAGGCGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2703
DB 2641 AAGGCGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694

RESULT 9

US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeggla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 ATCAAGAGTGTGAGTCCGAGCGGAGGAGGAGTCTGTAATCCGAGACCGCAGAGGAG 69
DB 1 ATCAAGAGTGTGAGTCCGAGCGGAGGAGGAGTCTGTAATCCGAGACCGCAGAGGAG 60
QY 70 GACGAGCTGTACTGTCTGGGCAACCGCGAGGACCACTTGTGTGGCGGCGGTGGCTTG 129
DB 61 GACGAGCTGTACTGTCTGGGCAACCGCGAGGACCACTTGTGTGGCGGCGGTGGCTTG 120

QY 130 AAGGAGACCCGCGGAGGAGACGAGGAGGAGCCGGATGAGCTGTCTGGGAAAGCCGCTCT 189
DB 121 AAGGAGACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 130 TACAGAGTACGACAAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 249
DB 181 TACAGAGTACGACAAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 250 TACAGAGTACGACAAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309
DB 241 TACAGAGTACGACAAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 310 CTGTCTTTGCTGTGCTTGAATTTTGTCAAGTGTCTTCAATCCCTGACGACACAAATTTG 369
DB 301 CTGTCTTTGCTGTGCTTGAATTTTGTCAAGTGTCTTCAATCCCTGACGACACAAATTTG 360
QY 370 GCGTCAAGTGTGCTGTGATCTGTGAGTTCGATGATGATGATGATGATGATGATGATGAT 429
DB 361 GCGTCAAGTGTGCTGTGATCTGTGAGTTCGATGATGATGATGATGATGATGATGATGAT 420
QY 430 ATCATTCGAATCTGTGCGGAGTGTGCTGTGATGATGATGATGATGATGATGATGATGAT 489
DB 421 ATCATTCGAATCTGTGCGGAGTGTGCTGTGATGATGATGATGATGATGATGATGATGAT 480
QY 490 AGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTATGCTTCAATAGCA 549
DB 481 AGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTATGCTTCAATAGCA 540
QY 550 GTTGTCTGCAAAACCTGAGGATATATTTTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 609
DB 541 GTTGTCTGCAAAACCTGAGGATATATTTTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 600
QY 610 TTCTTACAGATCTCTCGAGTGTGCGCATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAG 669
DB 601 TTCTTACAGATCTCTCGAGTGTGCGCATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAG 660
QY 670 GGTGAGTGTGTATGCTTACAGCAAGGATATATCAAGTGTGCAAGTGTGCAAGTGTGCA 729
DB 661 GGTGAGTGTGTATGCTTACAGCAAGGATATATCAAGTGTGCAAGTGTGCAAGTGTGCA 720
QY 730 GTTCTTATTTTGTGCTTCTCTCTGCTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 789
DB 721 GTTCTTATTTTGTGCTTCTCTCTGCTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 790 TCTACATATGACAGATCTCTGAGTGTGAGGAGCAATTTAATGACATTAATTTGCTATG 849
DB 781 TCTACATATGACAGATCTCTGAGTGTGAGGAGCAATTTAATGACATTAATTTGCTATG 840
QY 850 GACAAAACTCCCTTACATTTGCTGTGAGGAGATTTGCTTGTGAGGCTTGTGCACTCTTGGC 909
DB 841 GACAAAACTCCCTTACATTTGCTGTGAGGAGATTTGCTTGTGAGGCTTGTGCACTCTTGGC 900
QY 910 ATTCTTCTTTGCACTTCTGCGGAGGAGTCTGTGCTGAGTGTGCAATTTAAGTACAA 969
DB 901 ATTCTTCTTTGCACTTCTGCGGAGGAGTCTGTGCTGAGTGTGCAATTTAAGTACAA 960
QY 970 GAAACAACCCGCGACAAACACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1029
DB 961 GAAACAACCCGCGACAAACACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
QY 1030 TGTGTTTGGCTGTATGTTAGGAGCTGATGAGAAATCTGTTTGCATTTGCAACCTGGAAGCA 1089
DB 1021 TGTGTTTGGCTGTATGTTAGGAGCTGATGAGAAATCTGTTTGCATTTGCAACCTGGAAGCA 1080
QY 1090 CACTTGAAGGCTTGTGACACCTGAGGCTTGTGCAAGAAAGAAAGAAAGAAAGAAAGAAAG 1149
DB 1081 CACTTGAAGGCTTGTGACACCTGAGGCTTGTGCAAGAAAGAAAGAAAGAAAGAAAGAAAG 1140
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DB 1141 AGTCAAGAGCTAAGTTTAAAGAGGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTG 1200
QY 1210 AAGAGCCGACAAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1269

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1270 GGCAGTCCCAACCAAGTGACAGAGAGCTGGAGCTTCAACGACCCGCTTCCGGCCC 1329
1261 GGCAGTCCCAACCAAGTGACAGAGAGCTGGAGCTTCAACGACCCGCTTCCGGCCC 1320
1330 TCGGTGGCCCTCAAAAGTTCTCAGCCGCAAAACAGTGTATAGTGTGACAGAGCCCTTGGC 1389
1321 TCGGTGGCCCTCAAAAGTTCTCAGCCGCAAAACAGTGTATAGTGTGACAGAGCCCTTGGC 1380
1390 ACTGATGATGATATGATGTAAGAAAAGATGCGCAGTGTATGATCAGTGAAGACCTCACC 1449
1381 ACTGATGATGATATGATGTAAGAAAAGATGCGCAGTGTATGATCAGTGAAGACCTCACC 1440
1450 CCACCACTTAAACTGTGATTCGAGCTATCAGAAATTATGAAATTTCACTGTTGCAAAACGG 1509
1441 CCACCACTTAAACTGTGATTCGAGCTATCAGAAATTATGAAATTTCACTGTTGCAAAACGG 1500
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1501 AAGTTTAAGGAAACGTTACGTCATATGATGTAAAGATGCAATGCAATATTCCTGCT 1560
1570 GGTCTATGACATGTTGTGTAGATTTAAAGCCTTCAAAACAGCTGTTGATCAAAATTTCTT 1629
1561 GGTCTATGACATGTTGTGTAGATTTAAAGCCTTCAAAACAGCTGTTGATCAAAATTTCTT 1620
1630 GGAAGAGGCAAAATCAGATCAGATAGAGAGCCGAGAGAAATTAACAGACAGAACTAGAG 1689
1621 GGAAGAGGCAAAATCAGATCAGATAGAGAGCCGAGAGAAATTAACAGACAGAACTAGAG 1680
1690 ACCACAGACATCTCAGTATGCTCGTGGGTGTGTAAGTTGAAAAACAGTACAGTCC 1749
1681 ACCACAGACATCTCAGTATGCTCGTGGGTGTGTAAGTTGAAAAACAGTACAGTCC 1740
1750 ATAGAAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTCCGAAAGGCTCT 1809
1741 ATAGAGTCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTCCGAAAGGCTCT 1800
1810 GCTCAGCCCTCGCTTTGGCTTCACTTCAGTTCGACCTTTTGAAATGTAACAGACATCT 1869
1801 GCTCAGCCCTCGCTTTGGCTTCACTTCAGATCCCACTTTTGAAATGTAACAGACATCT 1860
1870 GACTATTAAGAGCCCTGTGTAGTAAAGATCTTTCCGGCTTCCGACAAACAGTGGCTGC 1929
1861 GACTATTAAGAGCCCTGTGTAGTAAAGATCTTTCCGGCTTCCGACAAACAGTGGCTGC 1920
1930 TTATCCAGATCACTAGTGCACACATCTCGAGAGAGCCCTGAGGTTCACTTGTGAGCCCAAT 1989
1921 TTATCCAGATCACTAGTGCACACATCTCGAGAGAGCCCTGAGGTTCACTTGTGAGCCCAAT 1980
1990 GAGTTCAGTCCCGAGACTTTTCTAGCGGCTTAGCCCTAATGCAAGTCAAGCAACAGAG 2049
1981 GAGTTCAGTCCCGAGACTTTTCTAGCGGCTTAGCCCTAATGCAAGTCAAGCAACAGAG 2040
2050 GTGCGCAATTAGTCAAAAGCGATGGTCTGACAGTGGCAGCAACCAACATATGCAAAACAA 2109
2041 GTGCGCAATTAGTCAAAAGCGATGGTCTGACAGTGGCAGCAACCAACATATGCAAAACAA 2100
2110 ATAAATACGGGACCCAGGACGAGCCCAACAACTTTAAGATCCCACTCTCTCTCCCA 2169
2101 ATAAATACGGGACCCAGGACGAGCCCAACAACTTTAAGATCCCACTCTCTCTCCCA 2160
2170 GCCATCAAGCATCTGCCAGGCGCAAAACTCTGACCCCTAACCCTGAGGCTTACAGAA 2229
2161 GCCATCAAGCATCTGCCAGGCGCAAAACTCTGACCCCTAACCCTGAGGCTTACAGAA 2220
2230 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCCAAGGAAATGTTCAAGTGTGACAG 2289
2221 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCCAAGGAAATGTTCAAGTGTGACAG 2280
2290 TCAAACTCAACCAAGGACCGTTCTATGAGAAAAGCTTTGACATGAGGAGGAAACTCTG 2349

2281 TCAAACTCAACCAAGGACCGTTCTATGAGAAAAGCTTTGACATGAGGAGGAAACTCTG 2340
2350 TTGTCTGTCTGTCCCATGTTGCTCCGAAAGGACTTGGGCAATCTTTGTCTGTGAAAACTTG 2409
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2410 ATCAGGTGACGAGGAAATGTAATATACAACTTTGAGGAGTGTCAAGTGGCTCAGA 2469
2401 ATCAGGTGACGAGGAAATGTAATATACAACTTTGAGGAGTGTCAAGTGGCTCAGA 2460
2470 GGCAGGCAAGATTTTACCCTCAAAATGAGGAAATCCAAATGTTTAACTGATGAAGAG 2529
2461 GGCAGGCAAGATTTTACCCTCAAAATGAGGAAATCCAAATGTTTAACTGATGAAGAG 2520
2530 GTGGGTCCTCCGAAAGACAGAGACAGCACTTTTGAATGCGCAGCCGAGCTTGCAGGGA 2589
2521 GTGGGTCCTCCGAAAGACAGAGACAGCACTTTTGAATGCGCAGCCGAGCTTGCAGGGA 2580
2590 GGTGCTTTGATCACTCTCTTAAAGACTGGAAGGTCAAGATCATCTCAGAGCAATTTGT 2649
2581 GGTGCTTTGATCACTCTCTTAAAGACTGGAAGGTCAAGATCATCTCAGAGCAATTTGT 2640
2650 AAGGACAGGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2703
2641 AAGGACAGGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2694

RESULT 10
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DMOREZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJANACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIEKOPF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCN05 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-948-493-1

Query Match 87.6%; Score 2690.4; DB 21; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

10 ATGAAGAGTGTGAGTTCGGGCGCGGCGAGGCTGCTGTAATCTCGGACGCGCGAGGGC 69
1 ATGAAGAGTGTGAGTTCGGGCGCGGCGAGGCTGCTGTAATCTCGGACGCGCGAGGGC 60
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61 GACGGCTGTGCTAGTGTGGGCAACCGCGGCGGCAAGCTTGTGGGCGGCGGCTGCTG 120
121 AGGGAAGCGCGCGGCGGCAAGGAGGCGGCGGATGAGCTGCTGTGGGGAAGCGGCTCT 180
130 AGGGAAGCGCGCGGCGGCAAGGAGGCGGCGGATGAGCTGCTGTGGGGAAGCGGCTCT 189
121 AGGGAAGCGCGCGGCGGCAAGGAGGCGGCGGATGAGCTGCTGTGGGGAAGCGGCTCT 180
190 TACACAGATGACCAAGCTGCGGCGCAACGTCAGTACCGGCGGCTGCAAACTACCTG 249
181 TACACAGATGACCAAGCTGCGGCGCAACGTCAGTACCGGCGGCTGCAAACTACCTG 240
250 TACACAGTGTGAGAGACCCCGGCGGCTGAGGCTTATCAACAGCTTGTGTTTCTC 309

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Db 241 TACAACTGCTGAGAGAGACCCCGGCTGGCGCTTCACTACCAAGCTTTGGTTTCTC 300
Qy 310 CTGTGCTTTGGTGTGCTGATTTTGTTCAGTGTTCCTTACCACTCCCTAGACACAAAATTG 369
Db 301 CTGTGCTTTGGTGTGCTGATTTTGTTCAGTGTTCCTTACCACTCCCTAGACACAAAATTG 360
Qy 370 GCCTCAAGTTGCTCTTGATCTCGAGTTGCGATGATGTCGTCTTTGGTTTGGAGTTC 429
Db 361 GCCTCAAGTTGCTCTTGATCTCGAGTTGCGATGATGTCGTCTTTGGTTTGGAGTTC 420
Qy 430 ATCATTCGAATCTGTGCTGCGGCTTCTGTTCGATATAGAGATGCGAAGAGACTG 489
Db 421 ATCATTCGAATCTGTGCTGCGGCTTCTGTTCGATATAGAGATGCGAAGAGACTG 480
Qy 490 AGGTTGCTCGAAGCCCTTGTGTATAGATACATTTGCTTTTCGCTTCAATAGCA 549
Db 481 AGGTTGCTCGAAGCCCTTGTGTATAGATACATTTGCTTTTCGCTTCAATAGCA 540
Qy 550 GTTGTCTTGCAGAAAACCTCAGGGTAATATTTTGGCAGCTGCACTCAGAACTCCGT 609
Db 541 GTTGTCTTGCAGAAAACCTCAGGGTAATATTTTGGCAGCTGCACTCAGAACTCCGT 600
Qy 610 TTCTTACAGATCTCCGCACTGTCGCGATGACCGAAGGGAGGCACTTGGAAATTACTG 669
Db 601 TTCTTACAGATCTCCGCACTGTCGCGATGACCGAAGGGAGGCACTTGGAAATTACTG 660
Qy 670 GGTTCAGGTTTATGCTCAGACAGAGAAATTAATACAGCTTGTGATCAATAGATTTTGG 729
Db 661 GGTTCAGGTTTATGCTCAGACAGAGAAATTAATACAGCTTGTGATCAATAGATTTTGG 720
Qy 730 GTTCTATATTTTTCGTCTTCTTCTGTCTATCTGTGAGAAAAGGATCCCAATAAGATT 789
Db 721 GTTCTATATTTTTCGTCTTCTTCTGTCTATCTGTGAGAAAAGGATCCCAATAAGATT 780
Qy 790 TCTACATATGAGATGCTCTGTGTGGGCAATTAATGCAATTAATGGCTATGGA 849
Db 781 TCTACATATGAGATGCTCTGTGTGGGCAATTAATGCAATTAATGGCTATGGA 840
Qy 850 GACAAAACCTCCCTTACCTTGGCTGGAGAGATTGCTTTCGAGGCTTTCACCTCCCTGGC 909
Db 841 GACAAAACCTCCCTTACCTTGGCTGGAGAGATTGCTTTCGAGGCTTTCACCTCCCTGGC 900
Qy 910 ATTTCTTTCTTGGACCTTCTGCGGCACTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 969
Db 901 ATTTCTTTCTTGGACCTTCTGCGGCACTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 960
Qy 970 GAAACAACCGCGCAGAAAACCTTGGAAAAGAGAAACCCAGCTGCCAATCTCATTCAG 1029
Db 961 GAAACAACCGCGCAGAAAACCTTGGAAAAGAGAAACCCAGCTGCCAATCTCATTCAG 1020
Qy 1030 TGTGTTTGGCTGATGATGAGAGCTGATGAGAAATCTGTTCCATTGCAACTGGAAGCA 1089
Db 1021 TGTGTTTGGCTGATGATGAGAGCTGATGAGAAATCTGTTCCATTGCAACTGGAAGCA 1080
Qy 1090 CACTTGAAGGCTTGGACACTGACAGCCCTTACCAAGAAAAGAAACAAGGGAGCATCAAGC 1149
Db 1081 CACTTGAAGGCTTGGACACTGACAGCCCTTACCAAGAAAAGAAACAAGGGAGCATCAAGC 1140
Qy 1150 AGTCAGAACTAAGTTTAAAGAGCAGATGCGCATGCTTACGCCCAAGGGGCAAGATATT 1209
Db 1141 AGTCAGAACTAAGTTTAAAGAGCAGATGCGCATGCTTACGCCCAAGGGGCAAGATATT 1200
Qy 1210 AAGAGCGCAAGACCTCAGATGATGACAGAGGTTCCCAAGCAGCAATCAAGCCGAG 1269
Db 1201 AAGAGCGCAAGACCTCAGATGATGACAGAGGTTCCCAAGCAGCAATCAAGCCGAG 1260
Qy 1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGCTTCCGCCC 1329
Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGCTTCCGCCC 1320
Qy 1330 TGGCTGCGCTCAAAAGTTCTCAGGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1389
|||||

Db 1321 TGGCTGCGCTCAAAAGTTCTCAGGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1380
Qy 1390 ACTGATGATGATATAGAGAAAAGATGCCAGTGTGATGATTCAGTGGAAACCTCACCC 1449
Db 1381 ACTGATGATGATATAGAGAAAAGATGCCAGTGTGATGATTCAGTGGAAACCTCACCC 1440
Qy 1450 CCACACCTTAAACCTGTCACTTGCAGCTATCAGAAATTAAGAAATTCATGTTCAAAACGG 1509
Db 1441 CCACACCTTAAACCTGTCACTTGCAGCTATCAGAAATTAAGAAATTCATGTTCAAAACGG 1500
Qy 1510 AAGTTTAAAGAAACCTTACGTCATATGATGATTAAGAAATGTCATTTGAAACATATTTCTGT 1569
Db 1501 AAGTTTAAAGAAACCTTACGTCATATGATGATTAAGAAATGTCATTTGAAACATATTTCTGT 1560
Qy 1570 GGTTCATCGGACATGTTGTGATGATTTAAAGCCCTTCAACACGCTTGTATCAAAATTCCT 1629
Db 1561 GGTTCATCGGACATGTTGTGATGATTTAAAGCCCTTCAACACGCTTGTATCAAAATTCCT 1620
Qy 1630 GGAAGAAAGGCAAAATCAGATCAGATTAAGAAAGCCGAGAGAAAATTAACAGCAGACATGAG 1689
Db 1621 GGAAGAAAGGCAAAATCAGATCAGATTAAGAAAGCCGAGAGAAAATTAACAGCAGACATGAG 1680
Qy 1690 ACCACAGACGATCTCAGATGCTCGGTGCGGTGTCAGAGTTGAAAACAGSTACATGCC 1749
Db 1681 ACCACAGACGATCTCAGATGCTCGGTGCGGTGTCAGAGTTGAAAACAGSTACATGCC 1740
Qy 1750 ATGAAATCCAAAGCTGGAATGCGCTACTAGACATCTATCAACAGGTCCTTCGAAAAGCTCT 1809
Db 1741 ATGAAATCCAAAGCTGGAATGCGCTACTAGACATCTATCAACAGGTCCTTCGAAAAGCTCT 1800
Qy 1810 GCTTCAGCCCTCGCTTTGGCTTCACTTCAGATTCACCACTTTTGAATGTAACAGACATCT 1869
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Qy 1870 GACTATCAAAAGCCCTGTGTGATGACAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC 1929
Db 1861 GACTATCAAAAGCCCTGTGTGATGACAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC 1920
Qy 1930 TTATCCAGATCAACATGAGCCCAACATCTCGAAGGCTCGCAGTTCAATCTGACGCGCAAT 1989
Db 1921 TTATCCAGATCAACATGAGCCCAACATCTCGAAGGCTCGCAGTTCAATCTGACGCGCAAT 1980
Qy 1990 GAGTTCAGTCCCAAGCTTTCTACGCGCTTACGCTTACATGACAGTCAAGCAACAG 2049
Db 1981 GAGTTCAGTCCCAAGCTTTCTACGCGCTTACGCTTACATGACAGTCAAGCAACAG 2040
Qy 2050 GTGCCAATTAATGTCAGAGAGATGCTCAGACATGTCGACCAACCAACATTTGCCAAACCA 2109
Db 2041 GTGCCAATTAATGTCAGAGAGATGCTCAGACATGTCGACCAACCAACATTTGCCAAACCA 2100
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Qy 2170 GGCATCAAGCATTTGCCAGGCGCAGAAAACCTTGACACCTTAAACCTTGACAGGCTTACAGAA 2229
Db 2161 GGCATCAAGCATTTGCCAGGCGCAGAAAACCTTGACACCTTAAACCTTGACAGGCTTACAGAA 2220
Qy 2230 AGCATTTTGAAGCTACCACTGCTTGTGTGCTTCCAAAGAAAATGTTCAAGTTGCAACAG 2289
Db 2221 AGCATTTTGAAGCTACCACTGCTTGTGTGCTTCCAAAGAAAATGTTCAAGTTGCAACAG 2280
Qy 2290 TCAAAATCTCAACCAAGAACGTTTCTATAGAGAAAAGCTTGAACATGAGAGAGAAAACCTGTG 2349
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Qy 2350 TTGTCTGTGTCTCCATGCTGTCAGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2409
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Qy 2410 ATCAGGTCGACCGAGGAACCTGAATATACATTTTCAAGGAGTGTGATCAAGTGGCTCCAGA 2469
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|||||

Qy	2470	GGGAGGCCAAGATTTTACC	CCAAAGGGAGGAATCCAAATTTGTTAATACGATGAAGAG	25229
Db	2461	GGAGCCAAAGATTTTACC	CCAAAGGGAGGAGATCAAAATTTGTTATATACGATGAAGAG	25202
Qy	2530	GTGGGTCCCGAAGACAGACAGACACTTTTGATGCGGACCGCAGCCTGCAGGGAA		25899
Db	2521	GTGGGTCCCGAAGACAGACAGACACTTTTGATGCGGACCGCAGCCTGCAGGGAA		25880
Qy	2580	GCTGCTTTGCATCAGACTCTCTTAAGACTGGAAGTCAAGATCATCTCAGAGCATTTGT		26499
Db	2581	GCTGCTTTGCATCAGACTCTCTTAAGACTGGAAGTCAAGATCATCTCAGAGCATTTGT		26480
Qy	2650	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAACATGAATTA		2703
Db	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAACATGAATTA		2694

RESULT 11
US-09-825-

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Sequence 1 Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedrich, Glenn
APPLICANT: Zamdrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2772
TYPE: DNA
ORGANISM: homo sapiens
IS-09-825-147-1

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Query Match	85.8%	Score 2635.4	DB 9	Length 2772
Best Local Similarity	98.9%	Pred. No. 0		
Matches 2673; Conservative	1	Mismatches 2	Indels 27	Gaps 1

QY	1	GGCAGCGGCATGAAGAGATGTGAGAGTCGGGACCGGGGACAGAGTGTCTGTAACTCCGGACACC	60
Db	97	GGCAGCGGCATGAAGAGATGTGAGAGTCGGGACCGGGGACAGAGTGTCTGTAACTCCGGACACC	156
QY	61	GCACAGGGGCGACCGGCTCTACTGTCTGGGACCCCGCGGGCCACGACTTGTGTTGGCGCGGC	120
Db	157	GCCAGAGGGCGACCGGCTCTACTGTCTGGGACCCCGCGGGCCACGCTCGATTGGCGCGGC	216
QY	121	GGTGGCCCTGAAGGAGAGCGCGCCGGGGCAAGCAGAGGGGGGCGCGGATAGCGTGTGGGGAAG	180
Db	217	GGTGGCCCTGAAGGAGAGCGCGCGGGGCAAGCAGGGGGGCGCGGATAGCGTGTGGGGAAG	276
QY	181	CCGCTCTCTTACACAGAGTAGCCAGAGCTTCGCGGCCAAGCTTCAAGTAACCGGCGGGTGCAG	240
Db	277	CCGCTCTCTTACACAGAGTAGCCAGAGCTTCGCGGCCAAGCTTCAAGTAACCGGCGGGTGCAG	336
QY	241	AACTACCTGTCAAAAGTGTGGAGAGACCCCGCGGCTGGGGGTTTATCTAACAGCGTTTC	300
Db	337	AACTACCTGTCAAAAGTGTGGAGAGACCCCGCGGCTGGGGGTTTATCTAACAGCGCTTTC	396
QY	301	GTTTTTCTCTCTTGTCTTGGTTGCTTGAATTTTGTCAAGTGTTTCTTACCAATCCCTGAGCAC	360
Db	397	GTTTTTCTCTCTTGTCTTGGTTGCTTGAATTTTGTCAAGTGTTTCTTACCAATCCCTGAGCAC	456

OY	361	ACAAAATTGGGCTCAAGTGTGCTCTGATATCTGGAGTTGCGATGATGTGCTGTTGGT	420
Db	457	ACAAAATTGGGCTCAAGTGTGCTCTGATATCTGGAGTTGCGATGATGTGCTGTTGGT	516
OY	421	TTGAGTTTCATCATTCGATATCTGTCTGCGGGTTCGTGTTGCAATATAGATGGCAA	480
Db	517	TTGAGTTTCATCATTCGATATCTGTGCTGCGGGTTCGTGTTGCAATATAGATGGCAA	576
OY	481	GGAAAGCTGAGATTGTGCTCGAAAAGCCCTTCGTGTATAGATATACATGTTCTTATGGCT	540
Db	577	GGAAAGCTGAGATTGTGCTCGAAAAGCCCTTCGTGTATAGATATACATGTTCTTATGGCT	636
OY	541	TCAAATAGCAGTGTGTTCTGCAAAAACCTCAGGGTATATTTTGGCAGCTCGCACTCAGA	600
Db	637	TCAAATAGCAGTGTGTTCTGCAAAAACCTCAGGGTATATTTTGGCAGCTCGCACTCAGA	696
OY	601	AGTCTCCGTTTCTTACAGATCTCTCCGATGGTGCGCATGCAACGAGGGAGGCACTTGG	660
Db	697	AGTCTCCGTTTCTTACAGATCTCTCCGATGGTGCGCATGCAACGAGGGAGGCACTTGG	756
OY	661	AAATTTACTGGGTTTACAGTGTATGTCACAGAAAGAAATTAATCACAGCTTGGTACATA	720
Db	757	AAATTTACTGGGTTTACAGTGTATGTCACAGAAAGAAATTAATCACAGCTTGGTACATA	816
OY	721	GGATTTTGGTCTTATATTTTTCGTCTTCCCTGTCTATCTGTGAGAAAGATGCCAAT	780
Db	817	GGATTTTGGTCTTATATTTTTCGTCTTCCCTGTCTATCTGTGAGAAAGATGCCAAT	876
OY	781	AAAGAGTTTCTACATATGACAGATGCTCTCTGTGTGGGGCAACAATTACTTACAACTATT	840
Db	877	AAAGAGTTTCTACATATGACAGATGCTCTCTGTGTGGGGCAACAATTACTTACAACTATT	936
OY	841	GGCTATGAGACAAAACCTCCCTTAACCTGTGGGAAAGATTGCTTTCGACGGCTTTGCA	900
Db	937	GGCTATGAGACAAAACCTCCCTTAACCTGTGGGAAAGATTGCTTTCGACGGCTTTGCA	996
OY	901	CTCCTTGGCATTTCTTCTTTTGCACTTCTGCGGCAATCTTGCTCAGATTTTGCAATTA	960
Db	997	CTCCTTGGCATTTCTTCTTTTGCACTTCTGCGGCAATCTTGCTCAGATTTTGCAATTA	1056
OY	961	AAAGTACAGAAACAACCGCCACAAAACCTTTAGAAAAGAAAGAACCCGAGCTGCCAAC	1020
Db	1057	AAAGTACAGAAACAACCGCCACAAAACCTTTAGAAAAGAAAGAACCCGAGCTGCCAAC	1116
OY	1021	CTCATTTCAGTGTGTTGGCGAGTATGCGACGCTGATGAGAAATCTGTTTCCATTTGCAAC	1080
Db	1117	CTCATTTCAGTGTGTTGGCGAGTATGCGACGCTGATGAGAAATCTGTTTCCATTTGCAAC	1176
OY	1081	TGGAAGCCACACTTGAAGGCTTTCGACACCTCGACGCCCTTACCAAGAAAGAACAGGGGAA	1140
Db	1177	TGGAAGCCACACTTGAAGGCTTTCGACACCTCGACGCCCTTACCAAGAAAGAACAGGGGAA	1220
OY	1141	GCATCAAGCAGTCAAGAGCTTAAGTTTAAAGAGGAGATGCGCATGGCTAGGCCAGGGGC	1200
Db	1221	GCATCAAGCAGTCAAGAGCTTAAGTTTAAAGAGGAGATGCGCATGGCTAGGCCAGGGGC	1269
OY	1201	CAGAGTATTAAGACCCCAACAAAGCTCTCAGTAGTGAACAGAGGTCTCCCAAGCATCGACATC	1260
Db	1270	CAGAGTATTAAGACCCCAACAAAGCTCTCAGTAGTGAACAGAGGTCTCCCAAGCATCGACATC	1329
OY	1261	ACAGCCGAGGGCAGTCCCAACCAAAAGTGAGAAAGAGCTTGAGACTTCAACGACCGAACCCGC	1389
Db	1330	ACAGCCGAGGGCAGTCCCAACCAAAAGTGAGAAAGAGCTTGAGACTTCAACGACCGAACCCGC	1449
OY	1321	TTCCGGGCCCTTCGTGCGCTCAAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACA	1380
Db	1390	TTCCGGGCCCTTCGTGCGCTCAAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACA	1449
OY	1381	GGCCTTGGACCTGATGATGATATAGATGAAAAGAGAGCCAGAGTGTATGATACAGTGGAA	1440
Db	1450	GGCCTTGGACCTGATGATGATATAGATGAAAAGAGAGCCAGAGTGTATGATACAGTGGAA	1509
OY	1441	GACCTCAACCCCAACTTAAACCTGTCATTCGACCTTACGAATTAAGAAATTCAGATTT	1500

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Db 1510 GACCTCACCCACACACTTAAACCTGTCATTCGAGCTATCAGAAATTGAAATTTTCATGTT 1569
Qy 1501 GCAAAACGGAAAGTTTAAAGAAACRTTACGTCAATATGATGTAAATAATGATCATTTGAA 1560
Db 1570 GCAAAACGGAAAGTTTAAAGAAACRTTACGTCAATATGATGTAAATAATGATCATTTGAA 1629
Qy 1561 TATTCTGCTGTCATGTGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGTGTGAT 1620
Db 1630 TATTCTGCTGTCATGTGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGTGTGAT 1689
Qy 1621 CAAATTTCTTGAAAGGCAAAATCATCATGATTAAGAAAGCCGAGAGAAATTAAGACA 1680
Db 1690 CAAATTTCTTGAAAGGCAAAATCATCATGATTAAGAAAGCCGAGAGAAATTAAGACA 1749
Qy 1681 GAACATGAGACACAGACGATCTCAGTATGCTCGTCCGGTGGTCAAGGTTGAAAAACAG 1740
Db 1750 GAACATGAGACACAGACGATCTCAGTATGCTCGTCCGGTGGTCAAGGTTGAAAAACAG 1809
Qy 1741 GTACAGTCCATAGAAATCCAAAGTGA CTGCTTAAGACATCTATCAACAGGTCCTTCGG 1800
Db 1810 GTACAGTCCATAGAAATCCAAAGTGA CTGCTTAAGACATCTATCAACAGGTCCTTCGG 1869
Qy 1801 AAAGGCTTGCTCAGACCTCTGCTTGGCTTCACTTCAGTTCGACCTTTTGAATGTGA 1860
Db 1870 AAAGGCTTGCTCAGACCTCTGCTTGGCTTCACTTCAGATCCACCTTTTGAATGTGA 1929
Qy 1861 CAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGTCCGACAAAC 1920
Db 1930 CAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCCGGTCCGACAAAC 1989
Qy 1921 AGTGGCTGTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGATTCTTCTG 1980
Db 1990 AGTGGCTGTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGATTCTTCTG 2049
Qy 1981 AGCCCAAAAGATGTCAGTCCCAAGATTTCTAAGGCTTAAAGCCCTTAATGTGACAGTCA 2040
Db 2050 AGCCCAAAAGATGTCAGTCCCAAGATTTCTAAGGCTTAAAGCCCTTAATGTGACAGTCA 2109
Qy 2041 GCACACAGGTGCAATTAAGTCAAAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2100
Db 2110 GCACACAGGTGCAATTAAGTCAAAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2169
Qy 2101 GCACACAGGTGCAATTAAGTCAAAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2160
Db 2170 GCACACAGGTGCAATTAAGTCAAAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2229
Qy 2161 CCTTCTCCAGCCATCAAGATCTGCGGAGGCAAACTCTGACCTTAACCTGTGAGGC 2220
Db 2230 CCTTCTCCAGCCATCAAGATCTGCGGAGGCAAACTCTGACCTTAACCTGTGAGGC 2289
Qy 2221 TTACAGAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCAAGGAAATGTTTCAG 2280
Db 2290 TTACAGAGAAAGCATTTCTGACGTCACACCTGCTTGGCTTCAAGGAAATGTTTCAG 2349
Qy 2281 GTTGCAAGTCAAAATCTCAACAGACGCTTCTATGAGGAAAACTTTGACATGGAGGA 2340
Db 2350 GTTGCAAGTCAAAATCTCAACAGACGCTTCTATGAGGAAAACTTTGACATGGAGGA 2409
Qy 2341 GAAACTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2410 GAAACTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2469
Qy 2401 CAAACCTGATCAGTGCAGACCGAGAACTGAATATATCACTTTCAGGAGTGAAGTCAAGT 2460
Db 2470 CAAACCTGATCAGTGCAGACCGAGAACTGAATATATCACTTTCAGGAGTGAAGTCAAGT 2529
Qy 2461 GGCTCCAGAGGACGCAAGATTTTAAACCCCAATGAGGGAATCCAAATGTTTAACT 2520
Db 2530 GGCTCCAGAGGACGCAAGATTTTAAACCCCAATGAGGGAATCCAAATGTTTAACT 2589
Qy 2521 GATGAAGAGTGGGTCCGAAAGAGACAGACACTTTTGAATGCCGACCGACGCT 2580
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Db 2590 GATGAAGAGTGGGTCCGAAAGAGACAGACAGACACTTTTGAATGCCGACCGACGCT 2649
Qy 2581 GCCAGAGAGCTGCTTTGATCAGACTCTCTTAAGAGCTGAAAGTCAAGATCATCTCAG 2640
Db 2650 GCCAGAGAGCTGCTTTGATCAGACTCTCTTAAGAGCTGAAAGTCAAGATCATCTCAG 2709
Qy 2641 AGCATTTGTAAGGACGAGAAAGTACAGATGCTTCACTTGCCTCATGTCAAACTGAAA 2700
Db 2710 AGCATTTGTAAGGACGAGAAAGTACAGATGCTTCACTTGCCTCATGTCAAACTGAAA 2769
Qy 2701 TAA 2703
Db 2770 TAA 2772

RESULT 12
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803, 268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Query Match 85.8%; Score 2635.4; DB 19; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 GGCAGCGCATGAAGAGATGTGAGTGGGCGGCGGAGGCTGCTGTAACCTGGCAGCC 60
Db 97 GGCAGCGCATGAAGAGATGTGAGTGGGCGGCGGAGGCTGCTGTAACCTGGCAGCC 156
Qy 61 GGCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 157 GGCAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
Qy 121 GGTGGCTGAGAGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 217 GGTGGCTGAGAGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 276
Qy 181 CCGCTCTTTACAGAGTACGACGCTGCGGCGCAAGCTGTAAGTACCGGCGGCTGAG 240
Db 277 CCGCTCTTTACAGAGTACGACGCTGCGGCGCAAGCTGTAAGTACCGGCGGCTGAG 336
Qy 241 AACTACCTGTACAAAGTGTGAGAGACCGCGGCGTGGGAGTTTATCAACAGCTTTC 300
Db 337 AACTACCTGTACAAAGTGTGAGAGACCGCGGCGTGGGAGTTTATCAACAGCTTTC 396
Qy 301 GTTTTCTCTGCTTGTGTTGTTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360
Db 397 GTTTTCTCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 456
Qy 361 ACAAATTTGCGCTCAAGTGGCTTGTGATCCTGAGATTGATGATGTTGTTGTTGTTGTT 420
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Db 457 ACAAAATGGCTCAATGGCTCTTGTATCTGTGAGTTGCGATGATGATGCTGCTTGGT 516
Qy 421 TTGGAGTTCAATCATTCGATCTGTGCGGGTTGCTGTGTGATATAGAGATGGCAA 480
Db 517 TTGGAGTTCAATCATTCGATCTGTGCGGGTTGCTGTGTGATATAGAGATGGCAA 576
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Db 637 TCATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATATTTTGGCAAGTGTGACAG 696
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Qy 781 AAAGATTTTCTATCATATGAGATGCTCTCTGTGGGGCAAAATTAATTAAGCACTAAT 840
Db 877 AAAGATTTTCTATCATATGAGATGCTCTCTGTGGGGCAAAATTAATTAAGCACTAAT 936
Qy 841 GGGTATGAGACAAAACCTCCCTTAAGCTGAGTGGGGAATGCTTCTGAGGCTTTGCA 900
Db 937 GGGTATGAGACAAAACCTCCCTTAAGCTGAGTGGGGAATGCTTCTGAGGCTTTGCA 996
Qy 901 CTCCTTGGCAATTTCTTCTTGTGCACTTCTGCGGCAATCTTGGCTCAGGTTTGTGATA 960
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Qy 1021 CTCATTCAAGTGTGTTGGGCTAGTTAGCGAGCTGATGAGAAATCTGTTCCATTGCAACC 1080
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Db 1177 TGGAGCCACACTTGAAGGCTTGGCAACCTGCAAGCCTTACCAAGAAAGAAAGAAAGAA 1220
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Db 1270 CAGAGTATTAAGAGCCGAGCAAGGCTCAGTAGTGAAGAGGTCCTCCAGAGCAACGACATC 1329
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Db 1390 TTCGGGCTCTGCTGGGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGACACA 1449
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Db 1450 GGCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1509
Qy 1441 GACCTACCCCACTTAATAAATGTCATTCAGAGTATCAGAAATTAAGAAATTTCAATGTT 1500

Db 1510 GACCTACCCCACTTAATAAATGTCATTCAGAGTATCAGAAATTAAGAAATTTCAATGTT 1569
Qy 1501 GCAAAACGGAAGTTTAAGAAACRTTAAGCTCCATATGATGTAAGATGTCATTGAAACA 1560
Db 1570 GCAAAACGGAAGTTTAAGAAACRTTAAGCTCCATATGATGTAAGATGTCATTGAAACA 1629
Qy 1561 TATTCGCTGCTATGCAATGTTGTGTAGAAATTAAGAGCTTCAAAACAGTGTGAT 1620
Db 1630 TATTCGCTGCTATGCAATGTTGTGTAGAAATTAAGAGCTTCAAAACAGTGTGAT 1689
Qy 1621 CAAATTTCTGAAAAGGGGCAAAATCACATGATTAAGAGAGCCGAGAGAAATTAAGAGA 1680
Db 1690 CAAATTTCTGAAAAGGGGCAAAATCACATGATTAAGAGAGCCGAGAGAAATTAAGAGA 1749
Qy 1681 GAAATGAGACCAAGACATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1750 GAAATGAGACCAAGACATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1809
Qy 1741 GTACAGTCCATGAAATCCAAAGCTGAGCTGCTTATGAGATCATGATCAAGGTCCTTGG 1800
Db 1810 GTACAGTCCATGAAATCCAAAGCTGAGCTGCTTATGAGATCATGATCAAGGTCCTTGG 1869
Qy 1801 AAAGCTCTGCTCAGACCTCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 1870 AAAGCTCTGCTCAGACCTCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929
Qy 1861 CAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAC 1920
Db 1930 CAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAAC 1989
Qy 1921 AGTGGCTGCTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGGTTCAATTCG 1980
Db 1990 AGTGGCTGCTTATCCAGATCAACTAGTGCACATCTGAGAGGCTGAGGTTCAATTCG 2049
Qy 1981 ACGCCAAATGAATTCAGTCCGAGACCTTCTAAGCGCTTATAGCCTTATAGCAAGTCAA 2040
Db 2050 ACGCCAAATGAATTCAGTCCGAGACCTTCTAAGCGCTTATAGCCTTATAGCAAGTCAA 2109
Qy 2041 GCACACAGGTGCCAATTTAGTCAAAAGCATGCTCAGCAGTGGCAGCCCAACACATTT 2100
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Qy 2161 CCTTCCAGCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTGCAAGC 2220
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Db 2290 TTACAGAAAGCAATTTCTGAGCTCACACCTGCTTGTGCTTCCAGAGAAATGTTGAG 2349
Qy 2281 GTTGACAGTCAAAATCTCCAAAGGACGCTTCTATGAGAAAGCTTGAATGAGAGGA 2340
Db 2350 GTTGACAGTCAAAATCTCCAAAGGACGCTTCTATGAGAAAGCTTGAATGAGAGGA 2409
Qy 2341 GAAACTCTGTTGTCTGTCTGTCCATGCTGCCAGAGGACTTGGGCAAAATCTTGTCTGTG 2400
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Qy 2401 CAAAACCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCAAGGAGTGAATCAAGT 2460
Db 2470 CAAAACCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCAAGGAGTGAATCAAGT 2529
Qy 2461 GGCCTCAGAGGAGCAAGATTTTACCCCAATGAGAGGAAATCCAAATGTTTAACT 2520
Db 2530 GGCCTCAGAGGAGCAAGATTTTACCCCAATGAGAGGAAATCCAAATGTTTAACT 2589
Qy 2521 GATGAAGAGTGGTCTCCGAAAGAGACAGAGACAGACACTTTTGAATGCTGCGACCGAGCT 2580
Db 2590 GATGAAGAGTGGTCTCCGAAAGAGACAGAGACAGACACTTTTGAATGCTGCGACCGAGCT 2649

QY 2581 GCCAGGAAAGCTGCTTTGTCATGAGCTCTTAAGGACTGGAAGTCAAGATCATCTGAG 2640
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Db 2650 GCCAGGAAAGCTGCTTTGTCATGAGCTCTTAAGGACTGGAAGTCAAGATCATCTGAG 2709
QY 2641 AGCATTTGTAAAGGACAGAAAGTACAGATGCTTCACTGCTTGCCTCATGCTCAAACTGAAA 2700
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Db 2710 AGCATTTGTAAAGGACAGAAAGTACAGATGCTTCACTGCTTGCCTCATGCTCAAACTGAAA 2769
QY 2701 TAA 2703
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Db 2770 TAA 2772

RESULT 13

US-09-810-796-3
Sequence 3, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jeggla, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
US-09-810-796-3

Query Match 85.5%; Score 2626.4; DB 9; Length 2667;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
QY 10 ATGAAGATGTGAGTTCGGGCGGGGCGAGGAGTCTGCTGTAAGTCCGACAGCCGACAGGCG 69
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Db 1 ATGAAGATGTGAGTTCGGGCGGGGCGAGGAGTCTGCTGTAAGTCCGACAGCCGACAGGCG 60
QY 70 GACGGCTGCTACTGCTGGGACCCGCGCGGCGACGCTTGTGTGGCGGCGGCTGGCTTG 129
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Db 61 GACGGCTGCTACTGCTGGGACCCGCGCGGCGACGCTTGTGTGGCGGCGGCTGGCTTG 120
QY 130 AGGGAAGCGCGCGGGGCGAAGGAGGGGCGCGGATAGAGCTGCTGGGGAAGCCGCTCTCT 189
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Db 121 AGGGAAGCGCGCGGGGCGAAGGAGGGGCGCGGATAGAGCTGCTGGGGAAGCCGCTCTCT 180
QY 190 TACACAGTAGACAGAGCTGCGCGCGCAAGCTCAAGTACCGGCGGCTGCAGAACTACTG 249
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QY 850 GACAAATCTCCCTTAACTTGGCTGGGAAGATTGCTTTCGACAGCTTGGCACTCCCTGGC 909
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QY 1390 ACTGATGATGATATGATGAGAAAGAGATGCCAGTGTGATGATCATGATGAAAGACCTCA 1449
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Qy 1930 TTATCCGATCACTAGTGGCAACATCTCCGAGAGGCTCGACATTCATTCGAGCCCAAT 1989
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Db 2614 AAGGACAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATTA 2667

RESULT 14
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodini, Jacqueline
; APPLICANT: Rodrigue-May, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14295,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1120,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 33394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 55590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MP102-018P1RNMNMIM
; CURRENT FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-03-15
; PRIOR FILING DATE: 2002-03-15
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2002-04-29
; PRIOR FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-07-03
; PRIOR FILING DATE: 2002-07-03
; PRIOR FILING DATE: 2002-07-10
; PRIOR FILING DATE: 2002-07-10
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-23
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55

Query Match 16.9%; Score 518; DB 17; Length 2335;
Best Local Similarity 60.1%; Pred. No. 2.9e-139;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;
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QY 346 ACCATCCCTGAGCACAATAATTGGCTCAAGTTGCTCTGTAATCTGTGAGTTGCTGATG 405
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QY 586 AGCTCTGCACTGAGAGTCTCGGTCTCTAAGATCTCTCCGCAATGTTGGGCAATGACCA 645
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QY 1066 GTTTCATTGCACTGGAAGCACTTGAAGGCTTGCACACTGCAAGC----- 1116
DB 1160 GCTTACTGACAGCCACTGAGTACTATGACAGATCTCTCCATCTTTCAGAGAGCTG 1219
QY 1117 CTTACCAAGAAAGAAACAAGGAGAGATGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1161
DB 1220 GCTTCTTCTTGTGAGCAGTGAAGGAGCGGCGCAATGAGGAGCTTACGAGCTGAGAGTG 1279
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DB 1280 CGGCGGAGCGCGGTACCGGAGCAAGCTCCCGTTACCGCGCGGTGCGACCTGCCAC 1339
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DB 1340 CGGCGGAGAGCACTCTTCTGCTCTGAGGAAAGAGCGGATGGGATCAAAAGACCGC 1399
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DB 1460 ACAATGCGCACTCCCAAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1519

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DB 1862 AGGAAGCGCGGAG 1921
QY 1705 AGTATGCTGAGTGGGAGTGAAGGTTGAAGAAACAGATGATGATGATGATGATGATGATG 1764
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QY 1765 GACTGCTACTAGACATATCAACAGTCTTTCGAAAGGCTGCTGAGCCCTGCT 1824
DB 1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCG-----GCTGAGCACTCGGCAAGC 2035
QY 1825 TTGGCTTATTCAGTCTCCACCTTTTGAATGTAAGACAGATGATGATGATGATGATGATG 1884
DB 2036 CTGGGCGCGGAG 2095
QY 1885 GTGATGACAAAGATCTTTCGGGTTCCGACAAA 1918
DB 2096 GTGAGCAAGAGACATCTCCGCTCTCGCACAGA 2129

RESULT 15
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850, 928
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-10-850-928-1

Query Match 16.94; Score 518; DB 21; Length 2335;

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Db 1621 GGAAGAGGCAATATCACTCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGACATGAG 1680
Qy 1681 ACCACAGACATCTCAGATGCTCGGTGGGGGTCAAGGTTGAAGAAAACAGGTACAGTCC 1740
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Qy 1741 ATAGAGTCCAGCTGAGTGCCTACTAGACATCTATCAACAGTCTTCCGAAAGCTCT 1800
Db 1741 ATAGAGTCCAGCTGAGTGCCTACTAGACATCTATCAACAGTCTTCCGAAAGCTCT 1800
Qy 1801 GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACACATCT 1860
Db 1801 GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACACATCT 1860
Qy 1861 GACTATCAAGAGCCCTGAGATAGCAAAAGATCTTTGGGTTCCGACAAACAGTGGCTGC 1920
Db 1861 GACTATCAAGAGCCCTGAGATAGCAAAAGATCTTTGGGTTCCGACAAACAGTGGCTGC 1920
Qy 1921 TTATCAGATCAACTAGTCCCAACATCTCGAAGGCTCGCATTCATTCTGACGCCAAT 1980
Db 1921 TTATCAGATCAACTAGTCCCAACATCTCGAAGGCTCGCATTCATTCTGACGCCAAT 1980
Qy 1981 GAGTTCACTGCCCCAGACTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2040
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RESULT 2
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 ; Sequence 1, Application US/09813148
 ; Patent No. 6617131
 ; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHER, Christian
 ; APPLICANT: SCHERER, Constanze
 ; APPLICANT: SEBOHM, Guiscard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL, PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CNS
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813.148
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/194,041
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-813-148-1

Query Match 99.5%; Score 2681.2; DB 4; Length 3074;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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 Db 275 GAGGCGCTGCTAAGTGGGCAACCGCGGCGGCGGCTTGTGGCGGCGGCGGCTG 334
 QY 121 AGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
 Db 335 AGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 334
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 Db 395 TACACGATGAGCAGAGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 454
 QY 241 TACACGATGAGCAGAGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
 Db 455 TACACGATGAGCAGAGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 514
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 Db 515 CTGTCCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 574
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 Db 575 GCGTCAGATGCTCTTGTGATCTGAGATGATGATGATGATGATGATGATGATG 634
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 Db 635 ATCATTTGAATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694

QY 481 AGGTTTGTGGAAGAGCCCTTCTGTGTATATATATATATATATATATATATATAT 540
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 Db 1115 ATTTCTTTCTTGTGACATTTCTGCGGCAATTTCTTGTGAGGCTTGTGACATTT 1174
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 QY 1321 TCGCTGGGCTCAAAAGTTCTGACGCCAAACAGATGATGATGATGATGATGATG 1380
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 Db 1595 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1654
 QY 1441 CCACCACTTAAACCTGCTATGAGCTATCAAGATTAATTAATTTGATGCAAAACG 1500
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DB 1775 GGTGATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACAGTGTGTGTCAAATTCCT 1834
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1955 ATGAGATCCAGAGTGAAGTGGCTGCTAGAGATCTATCAACAGTCTCTTGGAAGGCTCT 2014
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2015 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGATCT 2074
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2135 TTATCCAGATCACTAGTGCACATCTGAGAGGCTGCAAGTTCATTCTGACGCCAAT 2194
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2195 GAGTTCAGTCCAGACCTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2254
2041 GTGCCAATTAATGACCAAGCGATGCTGACAGTGGCAGCCCAACCAACATTGCAACCA 2100
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2101 ATAAATACGGCAACCAAGCGATGCTGACAGTGGCAGCCCAACCAACATTGCAACCA 2160
2315 ATAAATACGGCAACCAAGCGATGCTGACAGTGGCAGCCCAACCAACATTGCAACCA 2374
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2495 TCAAATCTCAACCAAGACCGTCTTATGAGGAAAGCTTGAACAATGGGAGAGAACTCTG 2554
2341 TTGTCTGTCTGCTCCATGTGCGGAAGAACTTGGGCAAACTTTGTCTGTGCAAACTG 2400
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2401 ATCAGGTCCAGCAGAGAACTGAATATACAACTTTCAGGAGTGAATGAGTGCCTCACA 2460
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2675 GAGAGCAGAAATTTTACCACAAATGAGGGAATTCAAATGTTTAACTGAAGAG 2734
2521 GTGGGTCGCCAGAGACAGAGACAGACACTTTTGTATGTCGCAACCGAGGCTGCGAGGAA 2580
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2641 AAGGAGAGAAATGTAAGATGCTCAGCTTGTCAATGTCAAACTGAATAA 2694

DB 2855 AAGCAGAGAGAAATGTAAGATGCTCAGCTTGTCTCATGTCAAACTGAATAA 2908
RESULT 3
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
Query Match 97.4%; Score 2625.2; DB 4; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
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QY 1621 GGAAGAGGAGCAATCAGATCAGATTAAGAGAGCGGAGAGAAATTAACAGAGCAATGAG 1680
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QY 1801 GCTCAGCCCTGCTTTGGCTTCAATTCAGATCCCAACCTTTGAAATGTAAGACATCT 1860
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Db 1999 TTATCCAGATCAATATGTCACCAATCTTGAGAGGCTGTCAGATTCTTACGCCAAT 2058
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Db 2119 GTGCCAATTATGTCAAAGCGATGCTCAGCAGTGGAGCCAGCAACCAATTGCCAAACCA 2178
QY 2101 ATTAATACGACACCAAGCGAGCCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2160
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Db 2299 AGCATTTCTGAGTGCACCACTGCTTGTGCTCCCAAGAAATGTTGAGGTTGCACAG 2358
QY 2281 TCATATCTCAACAGAGACCGTTCTATGAGAAAGCTTTGACATGGAGAGAACTCTG 2340
Db 2359 TCATATCTCAACAGAGACCGTTCTATGAGAAAGCTTTGACATGGAGAGAACTCTG 2418
QY 2341 TTGTCTGTGTCCATGCTGTCGAGAGGAACTTGGGCAAACTTTGTCTGTGCAAAACCTG 2400
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Db 2479 ATCAGGTCGACGAGGAACTGAATATCAACTTTGAGGAGTGAAGTCAAGTGGCTCAGA 2538
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RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736

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; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehe, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sande, Arthur T.
; TITLE OF INVENTION: No. 676736e1 Human Ion Channel Protein and
; FILE REFERENCE: Lex-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-3

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Query Match      97.4%; Score 2625.2; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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QY 61 GAGGCGCTCTACTGCTGTGGGCAACCGCGCGCCACGCTTGATGGCGGCGGAGTGGCTTG 120
DB 225 GAGGCGCTCTACTGCTGTGGGCAACCGCGCGCCACGCTTGATGGCGGCGGAGTGGCTTG 284
QY 121 AGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 285 AGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 344
QY 181 TACACAGATGAGCAGAGTCCGCGCGCAACGTCATGATCCGAGGAGGAGGAGGAGGAGG 240
DB 345 TACACAGATGAGCAGAGTCCGCGCGCAACGTCATGATCCGAGGAGGAGGAGGAGGAGG 404
QY 241 TACACAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 405 TACACAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464
QY 301 CTGTGCTGTGGTGTGATTTTGTGATGATTTTGTGATGATTTTGTGATGATTTTGTGATG 360
DB 465 CTGTGCTGTGGTGTGATTTTGTGATGATTTTGTGATGATTTTGTGATGATTTTGTGATG 524
QY 361 GCGTCAGTGTGCTGTGATTCCTGAGATTCGATGATTCGATGATTCGATGATTCGATGAT 420
DB 525 GCGTCAGTGTGCTGTGATTCCTGAGATTCGATGATTCGATGATTCGATGATTCGATGAT 584
QY 421 ATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 480
DB 585 ATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 644
QY 481 AGGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 645 AGGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
QY 541 GTTGTGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 705 GTTGTGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 764
QY 601 TTCTTACAGATCTCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 765 TTCTTACAGATCTCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 824
QY 661 GGTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

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DB 825 GGTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 884
QY 721 GTTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 885 GTTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
QY 781 TCTACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 945 TCTACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004
QY 841 GACAAATCCCTTACCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 1005 GACAAATCCCTTACCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1064
QY 901 ATTCTTCTTGTGACCTTCTGCGGCAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 1065 ATTCTTCTTGTGACCTTCTGCGGCAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1124
QY 961 GAAACACACCGCAGAGAACCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1125 GAAACACACCGCAGAGAACCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1184
QY 1021 TGTGTTTGGCGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 1080
DB 1185 TGTGTTTGGCGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 1244
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QY 1141 AGTCAGAGCTTGAAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1280 --TCAGAGCTTGAAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1237
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DB 1338 AAGAGCGAGAACCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1397
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DB 1398 GAGAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457
QY 1321 TCGCTGCGCTGCAAAAGTTTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1458 TCGCTGCGCTGCAAAAGTTTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1517
QY 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1518 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577
QY 1441 CCACCACTTAAAGCTGATTCGAGCTATCAGAAATTAATGAAATTTGATGTTGCAAAACGG 1500
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QY 1501 AAGTTTAAAGAAAGCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
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DB 1698 GGTCACTGAGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1757
QY 1621 GGAAGAGGCAATATCATATCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1758 GGAAGAGGCAATATCATATCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1817
QY 1681 ACCACAGAGATCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
DB 1818 ACCACAGAGATCTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1877
QY 1741 ATGAGTCCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
DB 1878 ATGAGTCCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1937

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QY 1801 GCCTCAGCCCTGCTTGGCTTCAATCCAGATCCACCTTTGATGTGAACAGACATCT 1860
DB 1938 GCCTCAGCCCTGCTTGGCTTCAATCCAGATCCACCTTTGATGTGAACAGACATCT 1997
QY 1861 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1920
DB 1998 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 2057
QY 1921 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAGTTCAATTCGAGCCCAAT 1980
DB 2058 TTATCCAGATCACTAGTGGCAATCTCGAAGGCTGTGAGTTCAATTCGAGCCCAAT 2117
QY 1981 GAGTTGAGTCCAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
DB 2118 GAGTTGAGTCCAGACTTTCTAGCGGCTTACGCTTACTATGACAGTCAAGCAACAG 2177
QY 2041 GTGCCAATTAGTCAAAAGCATGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2100
DB 2178 GTGCCAATTAGTCAAAAGCATGCTCAGAGTGGCAGCCCAACCAACCATTTGCAACCA 2237
QY 2101 ATTAATACGGACCCCAAGCCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA 2160
DB 2238 ATTAATACGGACCCCAAGCCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA 2297
QY 2161 GCCATCAGCATGCTGCCAGGCGCAAGAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2220
DB 2298 GCCATCAGCATGCTGCCAGGCGCAAGAACTCTGACCCCTAACCCCTGAGGCTTACAGGAA 2357
QY 2221 AGCATTTCTGACGTCAACCACTGCTTGTCTCTCCAGAGAAATGTTCAAGTTGACAG 2280
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DB 2418 TCAAATCTCAAGAGACGTTCTATGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2477
QY 2341 TTGTCGTCTGTGCCAATGCTGCGAAGGAATTTGGGCAATCTTGTCTGTGCAAACTCG 2400
DB 2478 TTGTCGTCTGTGCCAATGCTGCGAAGGAATTTGGGCAATCTTGTCTGTGCAAACTCG 2537
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DB 2538 ATCAGGTCCAGCAGAGAACTGAATATACACTTTCAGGAGTGAAGTCAAGTGGCTCAG 2597
QY 2461 GGCAGCCAGAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTAAGTGAAG 2520
DB 2598 GGCAGCCAGAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTAAGTGAAG 2657
QY 2521 GTGGGTCCGAAAGACAGAGACACTTTTGAATGCGCAGCCGACGCTGCGAAGGAA 2580
DB 2658 GTGGGTCCGAAAGACAGAGACACTTTTGAATGCGCAGCCGACGCTGCGAAGGAA 2717
QY 2581 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGGTCAGATCATCTCAGACATTTGT 2640
DB 2718 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGGTCAGATCATCTCAGACATTTGT 2777
QY 2641 AAGCAGAGAGAAAGTACAGATGCTTCAAGTTGCTTCAATGTAAGTAAATTA 2694
DB 2778 AAGCAGAGAGAAAGTACAGATGCTTCAAGTTGCTTCAATGTAAGTAAATTA 2831

RESULT 5
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823
Query Match 19.2%; Score 518.4; DB 4; Length 2196;
Best Local Similarity 60.1%; Pred. No. 1.2e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;
QY 217 TACCGCGGGTGACAGAACTACTGTAACAAGTGTGAGAGACCCCGCGGCTGGCTTC 276
DB 181 TACCGCGGGCTGACAGAACTGGGGTGAACGCTGTGAGAGCCCGCGGCTGGCTTC 240
QY 277 ATCTACAGCTTTCCTTCTCTTGTCTTGTGCTTGAATTTGTCAAGTCTTCT 336
DB 241 GTCTACAGCTCTCATATTTTGTCTGCTTCAAGTGTGCTGCTGCTGCTGCTGCT 300
QY 337 ACCATCCCTGACACACAAATTTGGCTCAAGTGTGCTTGTATCTGTGAGTTGATG 396
DB 301 ACTATCCAGAGACACCAAGAACTTGCACAGAGTCTCTCATCTTGAATTCGATG 360
QY 397 ATTGCTCTTGTGTTGAGTTCAATTCGATCTGTGCGGCTGCTGCTGCTGCTGCTG 456
DB 361 ATCTGCTTTTGGCTTGAAGTACATCTGCGGCTGTGCTGCGGCTGCTGCTGCTGCT 420
QY 457 TATAGAGATGCAAGAAAGAACTGAGTTGTCTGAAAGCCCTTGTGTTATGATACC 516
DB 421 TACCGAGATGCAAGGCTGCTTCCGCTTGCAGAAAGCCCTTGTGCTATGACACTTC 480
QY 517 ATTGCTCTTATGCTTCAATACAGTGTGTTGTGCAAAAACTCAGAGTAAATTTTGGC 576
DB 481 ATCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 577 ACCTGTCAGTCAAGAGTCTGCTTCTCTCAAGATCTCCGATGCTGCTGCTGCTGCTG 636
DB 541 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 637 AAGGAGAGCACTTGAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
DB 601 CGCGGCGCACTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 697 ACAGCTGTGATACATGAGATTTTGTGCTTATTTTGTGCTTCTTCTGCTGCTGCTG 756
DB 661 ACCGCTGTGATACATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 757 GAAAGATGCAATTAAGATTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTG 816
DB 721 GAGAGAGAGCAACTCCGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 817 ACATTGACAACTATTGCTATGAGACAAACTCCCTTAATCTGCTGCTGCTGCTGCT 876
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DB 841 GCTGCTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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DB 961 ATGCGCGAGCAACCTATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

QY 1057 GTTTCATTGCAACCTGGAAGCCACATTGAAGCCTTGACACTGACG----- 1107
Db 1021 GCCTACCTGACAGCCACTGTGTACTACTATGACAGTATCCTCCATCTTTGAGAGAGCTG 1080
QY 1108 CTTACCAAGAAAGAACAGAGGGAAGCATCAAGACATGACAAAGTA----- 1152
Db 1081 GCCCTCTTTGTTGAGACGTGCAACGGGCCCGCAATGGGGGCTTACGGCCCTGAGAGTG 1140
QY 1153 ----- 1152
Db 1141 CGGCGGGGCGCGGTACCCGACGAGCACTCCGTTACCCGCGCTTGACCTGCGCAC 1200
QY 1153 -----AGTTTAAAGAGCGA 1167
Db 1201 CGGCGGGGAGCAGCTCTTCTGCTGGGGAAGAGCGAGTGGGATCAAAAGACCGC 1260
QY 1168 GTGCGCATGGCTAGCCCGAGGGGCGA-----GTAATTAAGCCGACAGCCTGAGTA 1221
Db 1261 ATCCGATGGGCGCTCCAGCGCGAGGGGTCTTCCAGAGCATCTGGCAGCTTCA 1320
QY 1222 GGTGACAGAGGTCCCGCAAGCAGCATTCACAGCCGAGG---GCAGTCCCAACAAAGTG 1278
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Db 1435 -----AAACCCGCGACCTCTGTGAGATGCC---CTCAGAGAGAAATGAGCAGAG 1482
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QY 1459 ATTGAGCTATCAGAAATTGAAATTTCAATGTTGCAAAACGAAAGTTTAAAGAAAGTTA 1518
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QY 1519 CTTCCATATGATGTAAGAAATGATGATGTAACAATATTTGCTGTGTATCTGACATGTTG 1578
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QY 1579 TGTGAATTAAGAAAGCCTTCAACACGTGTTGATCAATTTCTGGAAGAAAGGCG---AAATC 1635
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QY 1756 GACTGCTACTAGACATCTATCAACAGGTCTTGGAAAGGCTGCGCTCAGCCCTCGGT 1815
Db 1843 GACCTGCTTGTGGGCTTTCTATTTCGGCTGCTGCG-----GCTTGGGCACTTGGGCGAGC 1896
QY 1816 TTGGCTTCAATTCAGATCCACCTTTTGAATGTAAGACAGACATCTGATATCAAGCCCT 1875
Db 1897 CTGGGGCGGTGCAAGTGGCGGTGTTGACCCCGACATCACTCGAGCTACACAGCCCT 1956
QY 1876 GTGATAGCAAAAGATTTTGGGGTTCGCAAAA 1909
Db 1957 GTGAGACAGAGACATCTCGTCTCCGACAGA 1990

RESULT 6
US-09-492-361-1
; Sequence 1, Application US/09492361

Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 19.2%; Score 518.4; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.3e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

QY 217 TACCGCGGGTGCAGAACTACCTGTACACGTGTGAGAGACCCCGCGCTGGCGCTTC 276
Db 320 TACCGCGCGCTGCAGAACTGGGCTTACAAAGTGTGAGAGCGGCGCGGCGCTGGCGCTTC 379
QY 277 ATCTACACGCTTGTGTTTCTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 336
Db 380 GTCTACACGCTTCTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 439
QY 337 ACCATCCCTGAGACACAAAATGCGCTCAAGTTGCTTGAATCTGAGATCTGAGATCTGAGATG 396
Db 440 ACTATCAGAGACACAGAACTTGCACAGAGTGTCTCTCATTTTGAATTCGTGATG 499
QY 397 ATTGCTCTTTGTTGTTGAGTTTCATTCGAAATCTGCTGCGGTTGCTGTTGTTGTTGTTGTTG 456
Db 500 ATCGGTTTCTGCTGTTGAGATGATGTCGGGGTCTGTGTCGGCGGATGCTGCGCGC 559
QY 457 TATGAGATGAGCAAGAAAGTGAAGTTGCTGAAAGCCCTTGTGTTATAGATAC 516
Db 560 TACCAGAGATGAGAGGGTCTGCTTCCAGTTCAGAAAGCCCTTCTGTGATCAGACTTC 619
QY 517 ATTGTTCTTACGCTTCAATGAGATGTTCTGCAAAAACGAGGTAATATTTTGGC 576
Db 620 ATCGTTTCTGCTCTCGGTGCGCTCATGCGCGGGTACCGAGGCAATCTTCGCG 679
QY 577 ACCTGCACTCAGAAAGTCTCGTTTCTTCAAGATCTCCGATGTCGATGAGACGA 636
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QY 637 AGGGAGGCACTTGAATTAATGAGTTCAAGTGTGTTATGCTCACAGCAAGAAATTAATC 696
Db 740 CGCGCGGCACTTGAAGCTCTGGGCTCAAGTGTCTACGGGCAATGAGAGAGCTGATC 799
QY 697 ACAGTGTGATATAGATTTTGGTCTTATTTTGTCTTCTGTTCTGATATGATG 756
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QY 757 GAAAAGATGCAATTAAGATTTTCTACATATGAGATGCTCTCTGTTGGGCGCAAT 816
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QY 877 TCTGAGGCTTGTGACTCTGCTGATTTCTTCTTGTGACTTCTGCGCGGCAATCTTGGC 936
Db 980 GCTGCTGCTTGTGCTTATGAGGATCTCTTCTTGTGCTGCTGCGCGGCAATCTTGGC 1039

Oy	937	CCAGGTTTGGCATTTAAAGTACAAAGAACAAACCCGCCGAAACACTTTTGAGAAAAAGAG	996
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Oy	997	AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGACAGCTGATGAAATCT	1056
Db	1100	ATGCCGGAGCGCAACTCATTCAGAGCTGGCTGGCCCTGTACTCCACCGAATATGAGCCGG	1158
Oy	1057	GTTTCCATTGGCACTTGGAAAGCCACACTTTGAAGGCTTGCACACTGCAAC	1107
Db	1160	GCTTACCTGACAGCCACCTGTGATCATATGACAGTATCTTCCATCTTTCAGAGAGCTG	1219
Oy	1108	CCTACCAAGAAAGAACAAAGGGAGACATCAAGCAGTACGAAGCTA	1155
Db	1220	GCCCTCTTGTTTGAGCAGTGCACGGGCCGCAATGGGGCCTACGGCCCTTGAGGTG	1279
Oy	1153	-----	1152
Db	1280	CGGCGGGCGCGGTACCGGACGGAGCACCCCTCCGTTACCGCGCGGTTGCCACTGGCAC	1338
Oy	1153	-----AGTTTAAAGACGA	1167
Db	1340	CGGCGGGCAGACCTCTTCTGCCCCGTGGGAAAGACAGCCGATGGGATCAAAAGACGC	1399
Oy	1168	GTGGCGATGGGTAGGCCCGAGGGGGCCAGA-----GTATTAAAGCCGACAAAGCCTCATTA	1221
Db	1400	ATCCGATGGGCGAGTCTCCAGGGGGGAGCGGGTCTTCCAAAGCAGACAGTGGCACTTCCA	1458
Oy	1222	GGTGACAGAGAGTCCCAAGCAGCCGACATCAAGCGCAGG---GGAGTCCCAACCAAGTG	1278
Db	1460	ACATGGCCCACTCCCAAGCAGCGAGCAGCAGGTGGGTGAGGCCACAGCCCAACCAAGGTG	1519
Oy	1279	CAGAAAGCTTGGAGCTTCAACGACCCGAAACCCGCTTCGGGCCCTGCTGCGCCTCAAAAGT	1338
Db	1530	CAAAAGAGCTGGAGCTTCAATGACCGGACCCGCTTCGGGACATCTTGAGACTC-----	1573
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Db	1574	-----AAACCCCGGACCTGTGCTAGAGATGCGC---CCTCAGAGAAAGTGAACAG	1621
Oy	1399	GAAAAAGATGCCAGTGTGATGTATCACTGGAAGACCTCACCCCACTTAAACCTGTC	1458
Db	1622	GAGAAAGACTACAGTGTGAGCTCACGGTGGACACATATGCTGCTGTGAAGACAGTC	1681
Oy	1459	ATTGAGCTATCAGAAATTATGAAATTTGATGTTGCAAAACGGAAGTTTAAAGAACTTAA	1518
Db	1682	ATCGGCTCATCAGGATTTCTCAAGTTCTGGGTGGCCAAAGGAATTCAGAGACACTG	1741
Oy	1519	CGTCCATATGATGTAAAGATGTCAATTGAACAATTTCTGCTGGTCATCTGACATGTTG	1578
Db	1742	CGACCGTACGACGTGAAGAGAGCTCAATTAGCAGTACTCAGACAGGCCCACTTGACATGCTG	1801
Oy	1579	TGTGAATTAAGGCTTCAAAACCGTGTATCAAAATTTGAAAAAGGGC---AATC	1635
Db	1802	GGCGGATCAAGAGCTGCAAACTGGGTGGACCAAAATTTGGGTGGGGGCGCGGGAC	1861
Oy	1636	ACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAACTATGAGACACAGACGATTC	1695
Db	1862	AGGAAGGCCGGGAGAAAGGGCGACAAAGGGGCCCTCCAGCGGAGGTGTGTGAATGTAATC	1921
Oy	1696	AGTATGCTCGGTGGGTGTGTAAGTTGAAAAACAGTACAGTCCATAGAGTCCAAAGTGTG	1755
Db	1922	AGCATGATGAGGACCGGTGTGTAAGGTGAGAAAGAGTGCAGTCCATCGACACAAAGCTG	1981
Oy	1756	GACATGCTACTAGACATCTATCAACAGGTCCCTTGGAAAAAGGCTGTGCTCAGCCCTGCT	1815
Db	1982	GACCTGCTTTGGGCTTTATTTGCGGCTGCGC-----GCTTGGGACCTCGGCGAGC	2035
Oy	1816	TTGGCTTCAATTCAGATCCCACTTTGAAATGTGAACAGATCGATATCAAAAGCCT	1875
Db	2036	CTGGGCGCGGTGCAAGTGCCTGTTGCAACCCCAATCACCTCCGATTCACACAGCCTT	2095
Oy	1876	GTGATAGCAAAAGATCTTTTGGGTTCCGACAAA	1909

Db	2096	GTGAGCACGAGCATCTCGCTCTCCGACAGA	2129
Query	Match	Score 516, DB 3, Length 2273;	
Best Local Similarity	57.6%; Pred. No. 6,4e-143;		
Matches 1030;	Conservative 2; Mismatches 684; Indels 72; Gaps 4;		
US-09-177-650-88			
Sequence 88, Application US/09177650			
Patent No. 6413719			
GENERAL INFORMATION:			
APPLICANT: Lepert, Mark F.			
APPLICANT: Singh, Nanda			
APPLICANT: Charlier, Carole			
TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE			
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)			
TITLE OF INVENTION: AND OTHER EPILEPSIES			
FILE REFERENCE: 2323-134			
CURRENT APPLICATION NUMBER: US/09/177,650			
CURRENT FILING DATE: 1998-10-23			
EARLIER APPLICATION NUMBER: 60/063,147			
EARLIER FILING DATE: 1997-10-24			
NUMBER OF SEQ ID NOS: 129			
SOFTWARE: Patent In Ver. 2.0			
SEQ ID NO 88			
LENGTH: 2273			
TYPE: DNA			
ORGANISM: Mus musculus			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)...(2271)			
US-09-177-650-88			

Db 607 TTGCAAACTCTTGCGATGATCCGATGACCGGAGGGGTGCACTTGAAAGCTCTTGGGA 666
Qy 664 TTAGTGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGATGACATATTTTGT 723
Db 667 TCGGTAGTCTAGCTCACAGCAAGAGCTGTGATCTGCTGTGATCACTTGGCTTCTCTG 726
Qy 724 CTATATTTTTCGTCCTTCTTGTCTATCTGTGAAAAGATGCAATAAAGATTTTCT 783
Db 727 CTCATCTGAGCCCTCATTTCTGTGTGACTTGTGCAAAAAGGTGATGATGACCATTTGAC 786
Qy 784 ACATATGAGATGCTCTGTGTGGGGGCAAAATTACATTTGACAACTATTTGGATAGAGAC 843
Db 787 ACCTAGCAGATGATCTGTGTGGGTCTGATCACCTTACGACCATGTGCTAGCGGAGC 846
Qy 844 AAAAATCCCCCTAATTTGGCTGGGAAAGATTTCTTTGACAGCTTTGCACTCTTGGCAT 903
Db 847 AAGTACCTTCAGACCTTGAAAGGAGCTGTGTGAGCAACCTTTCATCTTGTGTGTC 906
Qy 904 TCTTTCTTTGCACTTCTGCGGCAATTTCTGTGCTCAGGTTTGTGATTAAGTACAGAA 963
Db 907 TCGTTCTTTGCTTTCGCGCTGGCATTTTGGGATCCGCTTTCCTGAAGCTCAAGAG 966
Qy 964 CAACACCGCAGAAACATTTGAGAAAGAGAACCGCAGTGGCAACTTCATTCAGTGT 1023
Db 967 CAGCATCGGAAAAACATTTGAGAAACGCGGAAACCTGTGCGAGTCTGATCCAGTCT 1026
Qy 1024 GTTTGCGTATGTTTACCGAGCTGAT----- 1047
Db 1027 GCGTGGAGATTTGATGCTACTAACTCTGACGACCGACCTGACCTCAAGTGGAGTAC 1086
Qy 1048 ---GAGAAATCTGTTTCCATTTGCACTTGAAGCCCATTTGAAGCTTGTGACACTTGC 1104
Db 1087 TAGAGACGAACTGCTGTCTCCCATGTACAGCTCAAACTCAAACTATGGGGCTTCC 1146
Qy 1105 AG-----CCCTACCAAGAAAGAAAGAGGAGCATCAAGCATGCAAGGCTAAAGTTTA 1159
Db 1147 AGACTATCCCACTCTTGAACAGCTGAGCTGTGAGAAATTTCAAGCAAAATTTGGA 1206
Qy 1160 AAGAGAGATGCGCATGCTAGGCTCCAGGGGCGCAGATTTAAAGCCGCAAGCCTTCAG 1219
Db 1207 CTCACCTTGAAGAGAGGCAACAGGAGCATCAACAAAGCCCGAGGAGTGTGCTG 1266
Qy 1220 TAGGTACAGAGAGTCCCAAGACCGACATCAAGC----- 1256
Db 1267 AAGGGAAAGGGGTCTCCAGAGCCAGAGCTGCGCGGTCCCGCATGCGATCAGAT 1326
Qy 1257 --CGAGGGAGTCCCAAGAGTGCAGAAAGCTGAGCTTCAAGCCGAAACCGCTTC 1314
Db 1327 CTGTATGACAGCCCGAGCAAGGTGCCAAGAGCTTGTGTGATCCGCAAGCCGAC 1386
Qy 1315 CGGCGCTGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTATGATGCTGACACAGCC 1374
Db 1387 CGCAGAGCTTTCGCGATCAAGGGTGTGATCCCGCAGAAATTCAGAAAGAGCCCTC 1446
Qy 1375 CTGTGACATGATGATATATGTAAGAAAGATGCGAGTGTATCATGTGGAAGAC 1434
Db 1447 CTTGGGAGAGATCTGTAGAGCAACAAAGCTGAGCTGAGAGTTTGTGACTGAAGAT 1506
Qy 1435 CTCACCCCAACATTAACATGTCATTCGAGCTATCAGAAATTAATTAATTTTCATGTTGA 1494
Db 1507 CTTACCCCTGCGCTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1566
Qy 1495 AAACGAGATTTAAAGAAAGTTACGTCAATATGATGTAAGAAAGATGCTTGAACATAT 1554
Db 1567 AAGCGAAAGTTCAAAAGAGTGTGCGCCCATATGATGATGATGATGATGATGATGATGAT 1626
Qy 1555 TCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
Db 1627 TCGGCTGAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
Qy 1615 ATTCTTGAAAGAGGAGAAATCATCATGATTAAGAAAGCGAGAGAAATTAACAGAGAA 1674
Db 1687 ATTGTGGGGGGGGCCCAACATTAACGATTAAGAA--TCGACCAAAAGGCCCAAGCGAA 1743

Qy 1675 CATGAGACCAAGACATCTGATGCTCGGTGCGGTGTCAGGTTGAAAAACAGTGA 1734
Db 1744 ACGAGAGCTGCCGAAAGACCCAGATGATGGAGCGCTTGGGAAGGTGAGAAACAGTTC 1803
Qy 1735 CAGTCAATAGAGTCCAAAGCTGACTGCTACTAGCATCTATCAACAG 1782
Db 1804 TTGTCCATGAGAAAGAAAGCTGCACTTCTTGGTGAACATCTATACAG 1851

RESULT 8
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 18.9%; Score 510; DB 3; Length 2169;
Best Local Similarity 58.1%; Pred. No. 3.9e-141;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;

Qy 64 GGCCTGCTACTGCTGCGGACCGCGGCAACGCTTGTGTGGCGGCGGTGCTGAG 123
Db 67 GGCCTGCTGCGGCTGAGACCCGCGCGCCGACTTCAACAGCGAGCGGCTTACTATC 126
Qy 124 GAGAGCCCGCGGCGCAGCAGGGGCGCGATGAGCTGCTGAGGAGCCGCTCTTAC 183
Db 127 GCGGCTCCGAGGCGCCCAAGGCGGCGAGCGTTTGAACAAGCCGCGAGCGGCG 186
Qy 184 ACGATAGCCAGAGTGTGCGCGCGCAAGCTCAAGTACCGGCGGTGCAAACTACCTGATC 243
Db 187 GAGCGCGGAAAGCCCGCAAGCGCAACGCTTCTACCGCAAGCTGCAAAATTTCTCTAC 246
Qy 244 AACGTGTGAGAGAGACCCCGCGGCTGAGCTTCACTCAAGCTTGTGTTTCTCTT 303
Db 247 AACGTGTGAGAGAGAGCCCGCGGCTGAGCTTCACTCAAGCTTGTGTTTCTCTT 306
Qy 304 GTCTTGTGCTGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 363
Db 307 GTCTTGTGCTGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 366
Qy 364 TCAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
Db 367 GAGGGGCGCTTCACTATTTGAAATGTAAGTATGATGATGATGATGATGATGATGAT 426
Qy 424 ATTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
Db 427 GTGAGATCTGAGCTGAGGCTGCTGTTGCGGATGATGATGATGATGATGATGATGAT 486
Qy 484 TTTGTGCAAAAGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 543
Db 487 TTTGCAAGAAAGCGTTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 546
Qy 544 GTTTGTCAAAACCTCAGGATATATTTTGTGACAGTCTGACATCAGAAAGTCTCCGTTTC 603

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Db      547 CTGGCTCTGGTTCCTCCAGGGCAATGTCTTGGCAGCATCTGCGGCTCGGAGCTTGGGGTTC 606
Qy      604 CTACAGATCTCTCCGCAATGTCGCGATGAGACCGAAGGGGAGGACCTTGGAAATTAAGTGGT 663
Db      607 TTGGAAATCTTGGGAGATGATCCGTATGACCGGAGGGGTGGCACCTGGAAAGCTTGGGA 666
Qy      664 TCAGTGTATATGCTCAACAGAAATTAATCAACAGCTTGTATCATATGAGATTTTGGT 723
Db      667 TCGGTATCTACGCTCAACAGAAAGCTGTGATCTCCGTGTACATATGGCTTCTCTGC 726
Qy      724 CTATATTTTTCGTTCTTCTTCTGTATCTGTGAAAAAGATGCCAATAAAGATTTCT 783
Db      727 CTGATCTGGCTCATATTTCTGTGTACTGTGAGAAAAAGGTGAGATGACCACTTTGAC 786
Qy      784 ACATATGCAATGCTCTCTGTGGGGGCACAATTAATGACAACTATATGGCTATGAGAC 843
Db      787 ACCTAGCGAATGACATCTGTGGGGGTGTATCACTGACGACCAATTTGGCTACGGGGAC 846
Qy      844 AAAACTCCCTTAATTTGGCTGGGAAATGCTTTCTGACAGGCTTTTGCACTCTTGGCAT 903
Db      847 AAGTACCTTAGACCTGGAACGGGAGGCTGCTGGCAGCACCTTTACCTCATTTGGTTC 906
Qy      904 TCTTTCTTGGCACTTCTGCGGCAATTTGGCTCAGGTTTGCATTTAAAGTACAAGAA 963
Db      907 TCGTTCTTGTCTCTCTGCTGGCATTTTGGATCCGGCTTTGCGCTGAAAGTCCAAGAG 966
Qy      964 CAACACCGCCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTCCAACTCATTCAGTCT 1023
Db      967 CAGCATCGGAAAAACCTTTGAGAAACGGCGGAACCTTCGGCAGGTCTGATCCAGTCT 1026
Qy      1024 GTTTGGCGTAGTTACGCGAGCTGATGAGAAAT----- 1054
Db      1027 GCCTGAGATTTCTATGTACTTAACCTCTACGACCGACCTGCACTGACCTGACAGTAC 1086
Qy      1055 -----CTGTTTCATTGCAACCTGGAAGCCACACTTGAAGGCTTGCAC 1098
Db      1087 TACGAGCGACAGTCACTGTCCCATGTACAGACTCATCCACTGGAACAGCTGGAG 1146
Qy      1099 ACCTGACGCGCTTACCAAG-----AAGAACAGGGGAA 1131
Db      1147 CTGCTGAGGAATCTCAGAGCAAAATCTGACTCACTTCAGAAAGGACCAAGCAGAG 1206
Qy      1132 GCATCAGAGCAGTCAAGAGTAAATTTAAGAGGAG-----TGCGCATGCTTACCCCAAG 1188
Db      1207 CCATCACAAGTCAAGAGTCAAGTTTGAAGATGCTGTTCTTCCAGCCGCCAGGGCATG 1266
Qy      1189 GGGCAGATTTAAGAGCCGACAAAGCTCTAGTGTGACAGAGGTTCCCAAGCAGCAGAC 1248
Db      1267 GGTGCCAAGGAAAGGGGTCTCCCAAGGCCAGACGGTCCGGGGGTCCCAAGGGGAT 1326
Qy      1249 ATCACAAGCCGAGGCACTGCCACCAAGTGCAGAAAGCTGAGCTTCAACAGCAGAAC 1308
Db      1327 CAGAGTCTTGATACAGCCCGACAGAGTCCCAAGGCTGAGCTTTGGTGAAGCCAGC 1386
Qy      1309 CGCTTCGGGCTCTCGCTGCGCTCAAAAGTTCTCAGCCAAACAGATGATAGTGTGAC 1368
Db      1387 CGACACGCGAGGCTTCCGATCAGAGGTGCTGATCCGGCAGAAATTAAGAAAGCAGC 1446
Qy      1369 ACAGCCCTTGGCACTGATGATATATGATGAAAAAGATGCCAGTGTGATGAGTG 1428
Db      1447 C---TCCTGGGGAGGACATGTAAGAGCAACAGAGCTGTAAGCGAGTTTGGAGCT 1503
Qy      1429 GAAGACTCAACCCACCACTTAACCTGTATTCGAGCTTCAAGAAATTAAGAAATTTCA 1488
Db      1504 GAAGATCTTAACTCCCTGCGCTCAAGTTAGCATCAGAGCTGTGTGTATGAGCGTTCTTG 1563
Qy      1489 GTTGCAAAACGGAAGTTTAAGAAACGTTAGCTCATATGATGTAAGAAAGTGCATTGAA 1548
Db      1564 GTATCTTAAGGAAGTTCAAGAGAGCTCTGCCCATATATGATGAGACGTCATCGAA 1623
Qy      1549 CAATATTTCTGTCTGATCTGACATGTTGTGAAATTAAGACCTTCAACAGCTGTT 1608

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Db      1624 CAGTACTCGGCTGGACACTTGTGATGTGTGCCGATCAAGAGCCTGCGATCCAGAGTG 1683
Qy      1609 GATCAATTTCTTGGAAAAAGGCAATTCATCATGATTAAGAAAGCCGAGAAATTAACA 1668
Db      1684 GACCAATTTGTGGGCGGGGCCCAACAAATTAAGGATTAAGAA--TGCACCAAAAGGCCA 1740
Qy      1669 GCAGAAATGAGACACAGACGATCTCAGTATGCTCGTGGGTGTGCAAGTTGAAAAA 1728
Db      1741 GCGGAAAGGAGCTGCTCCGAAAGACCCACAGATGATGGAAGCGCTTGGAAAGTGGAGAA 1800
Qy      1729 CAGGTACGTCCATAGATTCACAGCTGAGCTGCTCTAAGACATCTATCAACAG 1782
Db      1801 CAGGTCTGTCCATGAGAAAGAGCTCGACTTCTTGGTGTGAGATCTATACAG 1854

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RESULT 9
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guejler, Karl, J.
; APPLICANT: Au-Yang, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

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Query Match      18.9%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      1621 GGAAGAGGCAATATCATCATATTAAGAGCCGAGAGAAATTAACAGACAGCATGAG 1680
Db      1 GGAAGAGGCAATATCATCATATTAAGAGCCGAGAGAAATTAACAGACAGCATGAG 60

Qy      1681 ACCACAGAGATCTCAGTATGCTCGGTGCGGTGTCAGAGTTGAAAAACAGGTACAGTCC 1740
Db      61 ACCACAGAGATCTCAGTATGCTCGGTGCGGTGTCAGAGTTGAAAAACAGGTACAGTCC 120

Qy      1741 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGATCTTCGAAAGGCTCT 1800
Db      121 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGATCTTCGAAAGGCTCT 180

Qy      1801 GCCTAGCCCTGCTTGGCTTATTCGATCCAGATCCCACTTTGAAATGTAAGAGACATCT 1860
Db      181 GCCTAGCCCTGCTTGGCTTATTCGATCCAGATCCCACTTTGAAATGTAAGAGACATCT 240

Qy      1861 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGCGGTTCCGCAAAACAGTGGCTGC 1920
Db      241 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGCGGTTCCGCAAAACAGTGGCTGC 300

Qy      1921 TTATCCAGATCACTAGTCCCAACATCTGAGAGGCTTGCAATTTCTGACGCCAAT 1980
Db      301 TTATCCAGATCACTAGTCCCAACATCTGAGAGGCTTGCAATTTCTGACGCCAAT 360

Qy      1981 GAGTTAGTCCAGACTTTTACAGGCTTACGCCCTACTATGACAGTCAAGCAACAGACAG 2040
Db      361 GAGTTAGTCCAGACTTTTACAGGCTTACGCCCTACTATGACAGTCAAGCAACAGACAG 420

Qy      2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGAGCCACCAACATTCGAAACCA 2100

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Db	421	GTGCAATTATGATCAAGCATGGCTTCAGATGCGAGCCACCAACCACTTGCACACCA	480
Qy	2101	ATAAATACGGCACCCAAGCCAGCAGCCCAACAATTTCAGATC	2145
Db	481	ATAAATACGGCACCAAGCCAGCAG-CCCAACAATTTCAGATC	524
RESULT 10			
US-09-105-058C-1			
; Sequence 1, Application US/09105058C			
; Patent No. 6403360			
GENERAL INFORMATION:			
APPLICANT: Blamar, Michael A.			
APPLICANT: Dworetzky, Steven			
APPLICANT: Gridkoff, Valentin K.			
APPLICANT: Levesque, Paul C.			
APPLICANT: Little, Wayne A.			
APPLICANT: Neubauer, Michael G.			
APPLICANT: Yang, Wen-Pin			
TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME			
FILE REFERENCE: 3053--4052			
CURRENT APPLICATION NUMBER: US/09/105,058C			
CURRENT FILING DATE: 1998-06-26			
PRIOR APPLICATION NUMBER: US 60/055,599			
PRIOR FILING DATE: 1997-08-12			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 1			
LENGTH: 896			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence:Consensus			
OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D			
OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;			
OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a			
US-09-105-058C-1			
Query Match 17.3%; Score 465.4; DB 3; Length 896;			
Best Local Similarity 53.7%; Pred. No. 4,4e-128;			
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2			
Qy	190	AGCCAGAGCTCCGCGCGCACTCAAGTACCGGCGGTCAGAACTACTGTACCAAGCTG	249
Db	13	RGSMS:CSMSYSAAAMGMAACCCCMWSTACCGSMSMS:CSARAMTTTSMTCACRACGS	72
Qy	250	CTGAGAGAACCCCGGGGCGTTCATCTACACACGCTTGCTTTCTCCGTGCTT	309
Db	73	CTRGAAGWRCSCSGGGCGGTGYSMTYACACGCGTSWGTGTTCTBTHDGYVTS	132
Qy	310	GTTGCTGATTTTCTAGTGTGTTCTACATCCCGACACACAATAATGGCTCAAGT	369
Db	133	KSSTCYBTRKCTKCTGTS-YKMCACAMTCAAGATATAGAGMKRKYTCBGRGRS	191
Qy	370	TGCTCTTGATCTCGAGTTGCTGATGATGTGCTGTTGTTGAGATTCAATTCGA	429
Db	192	KSSCTYYWSMTYTGGARAYMKTKCYATKTSRTVTTGGHGBAGTWKYKTMGR	251
Qy	430	ATCTGCTGGGGGTTGCTGCTGTGATTAAGATGCGCAAGAAAGTCAAGATGTGCT	489
Db	252	ATCTGGGCTGCGWGTGTYTSYCGCGRTACMWWGGCTGAGGAGGSGSRCTSAAGTTGCG	311
Qy	490	CGAAAGCCCTTCTGTATTATAGATACATTTGTTTATGCTTCAATACAGATGTTTCT	549
Db	312	MGAARCCVCTSTGYRTGWTBAYATCMTWKGTGCTSATYGCCTCYRKTCDGTGSKGY	371
Qy	550	GCAAAATCAAGGGTAAATATTTTGGCCAGCTGCATCAGAAGTCTCGGTTTCTACAG	609
Db	372	GYBGGHMMCCARGCGAAAGTYTKGTCYACVTCY---CTCBGAAGCTVGGSTTCYRRCAR	428
Qy	610	ATCTCCCGCATGTGTCCGATGAGCGGAAGGAGGAGCACTTGGAAATTACTGGGTTCAAG	669

Db	429	ATYTRCGSAAIGMTSCGBATGGACCGMGRGHGGCACTGGAACTBYTGGMCTDGV	488
QY	670	GTTATATGCTACAGAGAAATTAATCAACAGCTTGGTACATGATTTTGGTCTTATT	729
Db	489	RTCTRYGCVYACACCAARGARCTRTSCKGCSGTGTACATYGGYTTCTTBWSHCTCATC	548
QY	730	TTTTGCTCTTCCTTGCTCTATCTGTGGTGGAAAAAGATGCAATPAAGATTTTCTFCATAT	789
Db	549	CTKCKYCTRTTYCTKGGSTACTYGGYWWAPARARSDDGGRMBAGVSMWTTTGASACCTAY	608
QY	790	GCAGATGCTCTCTGGTGGGGACCAATTGACATGACAACTATTGGCTATGAGACAAACT	849
Db	609	GGRGATGCMCTSGTGGTGGGYCTGATACVCTGRVACATTTGGCTAYGGRGACAAGMMW	668
QY	850	CCCCTACTTGGCTGGGAAGATTGCTTTCTGACAGGCTTTGCACTGCTTGGCAATTTCTTTC	909
Db	669	CCYMARACSTGGRRMGGSGMGKCTHTDPCVCACTIYWCCTYMAITGGYGTCTCIVTYY	728
QY	910	TTTGCACTCTCGGCGGCGATCTTGGGCTCAGGTTTGGATTTGCAATTAAGTACAAAGAACACAC	969
Db	729	TTTGGBCCTCKMGCDGGCATIYTTGGGRCTCYGASITKGGCCCTSAARGTBCARAGACARAY	788
QY	970	CGCCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGGCAACCTCATTCAGTGTGTTTGG	1021
Db	789	MGKCARBARCACTTTGAGAAARMGGMGAABCCDDGCGMBRBTSATYCAKCKGKCCCTGG	848
QY	1030	CGTAGTTACGACGCTGA	1046
Db	849	AGRTWTAYGCIACYYAA	865

	RESULT 11	
/	Sequence 90, Application US/09177650	
/	Patent No. 6413719	
/	GENERAL INFORMATION:	
/	APPLICANT: Leppert, Mark F.	
/	APPLICANT: Singh, Nanda	
/	APPLICANT: Charlier, Carole	
/	TITLE OF INVENTION: KGN02 AND KGN03 - POTASSIUM CHANNEL GENES WHICH ARE	
/	TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)	
/	TITLE OF INVENTION: AND OTHER EPILEPSIES	
/	FILE REFERENCE: 2323-134	
/	CURRENT APPLICATION NUMBER: US/09/177,650	
/	CURRENT FILING DATE: 1998-10-23	
/	EARLIER APPLICATION NUMBER: 60/063,147	
/	EARLIER FILING DATE: 1997-10-24	
/	NUMBER OF SEQ ID NOS: 129	
/	SOFTWARE: PatentIn Ver. 2.0	
/	SEQ ID NO 90	
/	LENGTH: 2814	
/	TYPE: DNA	
/	ORGANISM: Mus musculus	
/	FEATURE:	
/	NAME/KEY: CDS	
/	LOCATION: (202)..(2811)	
/	US-09-177-650-90	
Query Match	17.2%; Score 464; DB 3; Length 2814;	
Best Local Similarity	57.9%; Pred.No. 2.5e-127;	
Matches 952; Conservative 3; Mismatches 623; Indels 66; Gaps 5		
OY	15 GTGGGCGGGGCAAGGCTGTGTAATCCGCCACGCCGCAGGGCGCAGCGCTGCTACT	74
Dd	294 GGCGGTGGCCGCGGCACGAGGAGCGGAAGTGGGCTGTGCGCCAGAGACGTGGACAAGT	353
OY	75 GCTGGGCAACC CGCGCGCACGCTTGTTGTGCGCGCGCGGTGAGCTGTGAGGAGAGCGCGCG	134
Dd	354 CACCTTGGCGGTAAAGGGCGCGAGCGCACAAAGAAGGAGACCCCTGCTCGTAGAGGGCGGTGG	413
OY	135 GGGCAGACGGGGGCGCGAATGAGCTGTCTGTGGGAAGCCGCTCTTTTACAGAGTAAGCCA	194
Dd	414 CCGGGAAGAGGGGAGAGAGAGAACCCGCGACAGGACATCGGGCTCTTCGCAAAAGACCCCT	473

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QY 195 GAGCTGCC-----GGCGAAGCTCAGATACCGGCGGGTGAGAGAACTACTGTTACA 245
    |||||
Db 474 GAGCCGCCCACTCAAGAGAAACAAGCCCAAGTACAGCGCATCAAACTTATCTATGA 533
QY 246 CGTCTGAGAGACCCCGCGGCTGGCGTTTCACTACACGCTTGTGTTTCTCTTGT 305
    |||||
Db 534 CGCCCTGGAAGACCGCGGGGCTGGGCGTGTCTACAGGCGCTGTGTCTGATTGT 593
QY 306 CTTTGTGTTGTTTGTTCATGTTTCTACCTTCCCTGAGACACAAATTTGGCCTC 365
    |||||
Db 594 CTTGGGATGCTTATTTCTGCGCGTGTCTACACCTTCAAGAAATAGAGCTGTCTGG 653
QY 366 AAGTGCCTCTTATCTGAGATTCGATGATTCGCTTGTGTTGGAGTTACAT 425
    |||||
Db 654 AGCTGCTTTTGTCTGTAAGAACATTTGCTATTTTCAATTTTGAAGCTGATTTGCTT 713
QY 426 TCGAATCTGCTTCGCGGTTCTGTTCGATATAGAGATGCGAAGAGACTGAGTT 485
    |||||
Db 714 GAGGATCTGGGCTGAGAGATGTTGCTGTGATCAAAAGCTGGCGTGAAGCTTAAAGTT 773
QY 486 TGTCTGAAAGCCTTCTGTGTTATAGATACCATTTCTTATGCTTCAATAGCACTGT 545
    |||||
Db 774 TGCAGAGAAAGCCCTGTGCAATGTGACATCTTCGATCTGATGCTGTGCAAGTGT 833
QY 546 TTCTGCAAAAACACAGGATAATTTTTCGCACTGCACTGAGAGTCTCGTTTCT 605
    |||||
Db 834 TCCCTGGGAAACAGAGGCATGCTTGGCACCT--CCCTCGAAGCCTTGTCTTCT 890
QY 606 ACAGATCTTCGCGATGATGCGCATGAGACCGAAGGGAGGCACTTGGAAATTAATGAGTT 665
    |||||
Db 891 GAGATCTGCGCATGCTTGAATGATAGAGGGGGTGGACCTGGAAGCTCTGGGGCTC 950
QY 666 AGTGGTTTATGCTCAAGCAAGAAATTAATCACAGCTTGTATATGATTTTGTCT 725
    |||||
Db 951 GGTATCTGTGCGCCACAGCAAGAAACTCATCACTGCTGTATAGAGTGGCTTCTGACAT 1010
QY 726 TATTTTGTGCTTCTGCTGTCTATGCTGTGAGAAAGATG----- 766
    |||||
Db 1011 CATCTTTCTTCTTCTTCTTCTTCTTCTGATGAGAAAGATGTCAGAAATGATGCCA 1070
QY 767 -----CCAAATAAGAGTTTCTATATATGAGATGCTCTGTGTGGGCAAT 815
    |||||
Db 1071 AGAGAGAGATGAAAGAGAGATTGAGACCTATGCAAGTCTCTGTGTGGGCTGAT 1130
QY 816 TACATTGACAACTATTTGGCTATGAGAACAACTCCCTTAACTTGTGCTGGAAGATTGCT 875
    |||||
Db 1131 CACACTGGCCACCATTTGTTATGAGACRAGACACTAAACCTGGGAAAGAGCTGTGAT 1190
QY 876 TTCTGAGGCTTTCGACTCCTTGGCACTTCTTCTTTCCTTTCCTGCGGGCACTTCTGG 935
    |||||
Db 1191 TGTCTGCACCTTTTCTTAAATGCGGCTCTCTCTTTTGGCCCTTCCGAGAGCACTTGG 1250
QY 936 CTCAGGTTTTCATTAAGATACAGAACACCGCCAGAAACACTTTTGAAGAAAGAG 995
    |||||
Db 1251 CTCAGAGACTGGGACTGAAGTTTCAAGAGAGACCGCTGAGAAACACTTTTGAAGAAAGAG 1310
QY 996 GAAACCAAGCTGCCAATCTTATTAAGTGTGTTTGGCTGATTAAGCACTGATGAGAAATC 1055
    |||||
Db 1311 GAAGCAGCTGCGGAATCTATTCAGGCTGCTGGAATATATATGATACCAACCCCAACAG 1370
QY 1056 TGTTCATTTGCAACCTGGAAGCCACACTTGAAGGCTTGCACACTGAGACCTTACCA 1115
    |||||
Db 1371 GTTGAATCTGTGTGCAACTGAGATCTTATGATCAATGTTGTCTTTTCCATTTCTTCA 1430
QY 1116 GAAAGAACAGAGGAAAGCATCAAGAGTCAAGAGTAAAGTTTAAAGAGAGATGGCAT 1175
    |||||
Db 1431 GAAAGAACAACTGGAAGACAGACAGCCAAAGCTGGGCTCTTGGATCGGGTTGCGCT 1490
QY 1176 GGTACGCCAGAGGGGCAAGATTTTAAAGCCGACAGCTCAATGATGAGAGAGAGTTC 1235
    |||||
Db 1491 TTCTAATCTCTGTTGAGCAATTA-----AGAAAGCTATTTAG 1532

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QY 1236 CCAAGACACGACATCATACAGCCGAGGCGATGCCCAAAAGTGAGAGAGCTT 1295
    |||||
Db 1533 CCTCTGAATGTAGATGCTATGAAAGAAAGCCCTTCCAAAGGCCAAAGCCTTGGCTT 1592
QY 1296 CAACGACCAAGCCGCTTCCGCGCCTCGCTGCGCTCAAAAGTTCTCAGCCAAACAGT 1355
    |||||
Db 1593 AAAACAATAAAGAGCGTTTCCGACCGCTTCCGATGAAAGGCTACGCTTTCGAGAG 1652
QY 1356 GATAGATGCTGACACAGCCCTTGGCACTGATATATATATGATGAAAGATGCCAGTG 1415
    |||||
Db 1653 WTCTGAAGATGTGGGACAGGAGCC-----CATGGCAAGACAGGGGCTATGGGA 1706
QY 1416 TGATGATCAGTGAAGAGACCTCACCCACCACTTAAATGTCATTCGATGATGAGAT 1475
    |||||
Db 1707 TGAATCTCTCATTTGAAGACATATCTCTTCCCTTAAAGCTGCAATCCAGCTGTCAAGAT 1766
QY 1476 TATGAATTTCAATGTTGCAAAACGAAAGTTTAAAGAAAGTTACGTCAATATGATAA 1535
    |||||
Db 1767 TCTACAGTTCCGTCTATATATAAAGAAAGTTCAAGAGAGAGCTTGAAGCCTTATGATGAA 1826
QY 1536 AGATGCTATGAACAATATTTCTGCTGTGATCTGACATGTTGTGTAGAAATTAAGCT 1595
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Db 1827 AGATGATTTGACAGTATTTGCGCGGACATCTTGAACATGCTTTCAGGATTAAGTCT 1886
QY 1596 TCAACACGTTGATCAATTTCT 1619
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Db 1887 ACAGACAGAAATGATATGATTTT 1910
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RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamart, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIORITY FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

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Query Match      17.1%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 2.2e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

QY 13 GAGTGGGCGGGGAGAGGTTGCTGTGAATTCGAGAGCGCCAGGAGCGACCGCTGTGA 72
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Db 43 GGGGGGGGGCGGGGAGAGAGGAAAGTGGGGCTGGGCGCCGGGAGACGTGAGAGAA 102
QY 73 CTGCTGGGACACCCGCGCGCCACGCTTGTGTGGCGGCGCGGTGCTGAGAGAGAGCGC 132
    |||||
Db 103 GTCACTTTGGCCCTCGGGGCGAGACCGAACAGAGCCGATCTCTGTGAGGGCGCG 162
QY 133 CGGGGAGACAGAGGGGCGCGAGTGAAGCTTGGGGAAAGCGCTCTTACAGAGTGAAGC 192
    |||||
Db 163 GCGCGGAGAGAGGGGCAAGGAGAGACCCGCAAGGGCATGAGGCTCTTGGCCAAAGCCCC 222
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QY 193 CAGAGCTGCC-----GGCGAAGCTCAAGTACCGGCGGGTGAGAACTAATCTGTAC 243
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Db 223 CTGAGCGCCCAAGTCAAGAAACAGCCAGTACCGGCGCATCCAACTTTGATCTAC 282
Qy 244 AACGTCGTGAAGAGACCCGCGGCTGGGCGTTCATCTACACAGCTTTCGTTTTCTCTT 303
Db 283 GAGCGCTTGAAGAGACCGGCGGCTGGGCGCTCTTACCAAGCGTTGGTTCGATTT 342
Qy 304 GTCTTGTGTTGCTTGAATTTTGTCAAGTGTTCATCATCCCTGAGACAACAAATTGACC 363
Db 343 GTCTCTGGGGGTCTGTTGCTGCTGCTGACCACTTCAAGAGATATAGACTGCTCTG 402
Qy 364 TCAAGTGTGCTGTATCTGAGAGTGTGATGATGTGCTGTGTTTGAAGTTCATC 423
Db 403 GGAAGCTGCTCTGTATCTGAGACATTTGCTATTTTATCTTGGAGCCGATTTGCT 462
Qy 424 ATTGATCTGTGCTGCGGCTGCTGTGCTATATAGAGATGCGAAGAACTGAG 483
Db 463 TTGAGATCTGGGCTCTGATGATTTGCTGCGATACAAAGGCTGGGGCGGCTGAAG 522
Qy 484 TTTGCTGAAAGCCCTTCTGTGTTATATATATCATTTGCTTATCGCTTCAATAGCAT 543
Db 523 TTTGCGAGAGCCCTGCTGATGTTGACATCTTGTGCTGATGCTCTGTGCGCATG 582
Qy 544 GTTTCGCAAAAATCTAGGGTATATTTTGCAGCTGCACTGCAAGTCTCCGTTTC 603
Db 583 GTTCTGTGGAAACCAAGCAATGTTCTGGCCACT---CCCTGCAAGCCCTGGCGCTTC 639
Qy 604 CTACAGATCTCCGATGCTGCGATGACCGAAGGGAGAGCACTTGAATTAATCTGGGT 663
Db 640 CTGCAATCTCTGGCATGCTGCGGATGAGCCGAGAGGTGGCACCTGGAAGCTCTGGGC 699
Qy 664 TCAAGTGTATGCTACAGCAAGAAATTAATCAAGCTTGTGATATAGATTTTGGTT 723
Db 700 TCAAGCATGTGCTCCACAGCAAAAGCACTATCAGCGCTGGATACATCGGTTTCTGACA 759
Qy 724 CTATATTTTTCGCTTCTGCTGCTATCTGGTGAAGAAAGATGACC-----768
Db 760 CTATCTCTTCTTCTATTTCTGCTACCTGCTGTTGAAGAAAGCTCCCAAGGTGATGCA 819
Qy 769 -----AATAAGAGTTTCTACATATGACAGATGCTCTGCTGCTGGGACACA 813
Db 820 CAAGGAGAGAGATGAAGAGAGTTTGAAGACTATGAGATGCCCTGTGGTGGGCGCTG 879
Qy 814 ATTACATTGACAACTATTGGCTATGGAAGCAAACTCCCTTAACCTTGGCTGGAGATTG 873
Db 880 ATCACACTGCGCCCACTTGTGCTATGAGACAGACACCCAAACGTTGGAGAGCCCTCTG 939
Qy 874 CTTTTCGAGGGCTTGCATCTCCCTGACATTTCTTTTGGACCTTCGCGGCAATCTT 933
Db 940 ATTGCGGCACTTTTCTTATTTGCGCTCTCTTTTGGCCCTTCCAGCGGGCATCTG 999
Qy 934 GGCTCAGTTTTCATTAATAAGTACAAAGACACCGCCAGAAACCTTTGAGAAAGA 993
Db 1000 GGGTCCGGGCTGGCCCTCAAGGTGAGAGCAACGTCAGAGACACTTTGAGAAAAAG 1059
Qy 994 AGGAACCCAGCTGCCAATCTATTCAGTGTGTTGGCGTATGTTACGACGTATGAGAAA 1053
Db 1060 AGGAAGCCAGCTGCTGAGCTCAATTCAGGCTGCTGAGGATATATGCTCAACACCCAAC 1119
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Db 1120 AGGATTTGACCTGTGGCGACATGAGATTTTATGATCAGTGTCTCTTTTCTTTCTTC 1179
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Qy 1174 ATGGCTAGCCCAAGGGGCGAGAGTATTAAGAGCCGCAAGCTCACTAGTATGACAGAG 1233
Db 1240 CTTTCTAATCTCTGTGTAGCATATA-----AGGAAAGCTATTT 1281
Qy 1234 TCCCAAGACAGCAATCAAGCCGAGGCGGACCCCAAAAGTGAAGAGAGCTGAGAC 1293
Db 1282 ACCCTCTGATGTAGATGCATAGAAAGATCTTCTTAAGAACCAAGGCTGTGGC 1341

Qy 1294 TTCAAGCACGAAACCCGCTTCGCGCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCA 1353
Db 1342 TTAAACATTAAGAGCGTTTCGACAGCGCTTCGCAATGAAAGCCT-----ACGCTTTC 1395
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Db 1396 TGGCAGAGTTCTGAAGATGCCGAGCAGGTGACCCCATGGGAGAGACAGGGGCTATGGG 1455
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Qy 1474 ATTATGAATTTGATGTTGCAAAACGAAAGTTTAAAGAAAGTTAAGTTCATATGATGTA 1533
Db 1516 ATTCTACATTCGCTCTATATAAAAAAATTCAGAGAGACTTTGAGGCTTACGATGTG 1575
Qy 1534 AAGATGCTATTGAACATATTTGCTGCTGCTCATCTGACATGTTGTATGAATTAAGAC 1593
Db 1576 AAGATGATGATGAGCAATATTTGCGCGGCAATCTGACATGCTTCCAGAGATAAGTAC 1635
Qy 1594 CTTCAACACGTTGATCAAAATCT 1619
Db 1636 CTTCAACAGAAATGATATGATTTT 1661

RESULT 13
US-09-177-650-6
Sequence 6, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2123-134
CURRENT APPLICATION NUMBER: US/09177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2914
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(2634)
FEATURE:
NAME/KEY: allele
LOCATION: (840)
OTHER INFORMATION: The polymorphism of a T to a C at this position
OTHER INFORMATION: has appeared in one individual.
FEATURE:
NAME/KEY: mutation
LOCATION: (947)
OTHER INFORMATION: The missense mutation from a G to a T occurs at
OTHER INFORMATION: this position in a BENC family.
FEATURE:
NAME/KEY: allele
LOCATION: (678)
OTHER INFORMATION: This position is polymorphic for C or T.
FEATURE:
NAME/KEY: allele
LOCATION: (750)
OTHER INFORMATION: This position is polymorphic for T or C.
FEATURE:
NAME/KEY: allele
LOCATION: (1089)
OTHER INFORMATION: This position is polymorphic for G or C.

FEATURE:
 : NAME/KEY: allele
 : LOCATION: (2598)
 : OTHER INFORMATION: This position is polymorphic for T or C.
 US-09-177-650-6

Query Match 17.1%; Score 460.8; DB 3; Length 2914;
 Best Local Similarity 57.9%; Pred. No. 2.4e-126;
 Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

QY 13 GAGTCGGGCGGGGCGAGGCTCTGAATCTGGCAGCCGCGAGGGCGACGCGCTTCTA 72
 DB 115 GCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 174
 QY 73 CTGCTGGGAGACCGCGCGCGCGCGAGCTTGTGGCGCGCGCGCGCGCTTGAAGAGAGCGC 122
 DB 175 GTCACTTGGCGCTCTGGGCGCGCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
 QY 133 CGGAGGAG 192
 DB 235 GCGCGCGAG 294
 QY 193 CAGAGCTGCC-----GCGCGAGAGTCAAGTACCGCGCGAGAGAGAGAGAGAGAGAG 243
 DB 295 CTGAGCGCGCGAGTCAAG 354
 QY 244 AAGCTGTGAG 303
 DB 355 GAGCGCTGAG 414
 QY 304 GTCTTGGTGTCTTGAATTTTGTCAAGTGTTCATCCCTGAGAGAGAGAGAGAGAGAGAG 363
 DB 415 GTCTGGGGGTCTTGAATTTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
 QY 364 TCAAGTGTCTTGAATTTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
 DB 475 GAGAGCTGTCTTGAATTTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
 QY 424 ATTGAATCTGTCTGTGGGTGTCTGTGTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
 DB 535 TTGAGAGATCTGTGGGTGTCTGTGTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
 QY 484 TTGCTCGAAG 543
 DB 595 TTGCGCAG 654
 QY 544 GTTTCGCAAAAATCAGGGTATATTTTTCAGAGCTGTCACTCAGAGATCTTCCGTTTC 603
 DB 655 GTTGTCTGTGGAAG 711
 QY 604 CTACAGATCTCGGAGATGTGGCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
 DB 712 CTGCAAGATCTCGGAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 771
 QY 664 TCAGTGTATATCTCAGACAG 723
 DB 772 TCAGCATCTGTGCGCAG 831
 QY 724 CTATATTTTTCGTTCTTCTGTCTATCTGTGTGAAAAGAGAGAGAGAGAGAGAGAGAG 768
 DB 832 CTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 891
 QY 769 -----AATAAGAGTTTCTACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
 DB 892 CAAG 951
 QY 814 ATTACATGACAACTATTTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
 DB 952 ATCACTGCGCAG 1011
 QY 874 CTTCCTGAG 933
 DB 1012 ATTGCGCGCAG 1071

QY 934 GGCTCAGGTTTNGCATTTAAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993
 DB 1072 GGGTCGGGCTGGCCCTCAAG 1131
 QY 994 AGGAGCCAG 1053
 DB 1132 AGGAG 1191
 QY 1054 TCTGTTTCCATTTGCAACCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1113
 DB 1192 AGGATGAGCTGTGTGAG 1251
 QY 1114 AAG 1173
 DB 1252 AGGAG 1311
 QY 1174 ATGGCTAGCCCGAG 1233
 DB 1312 CTTCCTATCTGTGTGAG 1353
 QY 1234 TCCCAAG 1293
 DB 1354 ACCCTCTGAG 1413
 QY 1294 TTCAAG 1353
 DB 1414 TTAAAG 1467
 QY 1354 GTGATGATGCTGAG 1413
 DB 1468 TGCCAG 1527
 QY 1414 TGTGATGATGCTGAG 1473
 DB 1528 AATGAGCTTCCCAATCAAG 1587
 QY 1474 ATTATGAATTTTCATGTTCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
 DB 1588 ATTCTCAATTTCCGTTCTTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1647
 QY 1534 AAGATGATGATGAG 1593
 DB 1648 AAGATGATGATGAG 1707
 QY 1594 CTTCAG 1619
 DB 1708 CTTCAG 1733

RESULT 14
 US-09-495-050A-305
 : Sequence 305, Application US/09495050A
 : Patent No. 6492505
 : GENERAL INFORMATION:
 : APPLICANT: Roopa, Reddy
 : APPLICANT: Guegler, Karl, J.
 : APPLICANT: Au-Yang, Janice
 : TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
 : FILE REFERENCE: PA-0013 US
 : CURRENT APPLICATION NUMBER: US/09/495, 050A
 : PRIOR FILING DATE: 2000-01-31
 : PRIOR FILING DATE: February 1, 1999
 : NUMBER OF SEQ ID NOS: 305
 : SOFTWARE: PERL Program
 : SEQ ID NO 305
 : LENGTH: 575
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : NAME/KEY: misc feature
 : OTHER INFORMATION: Incyte ID No. 6492505 4970006F6

NAME/KEY: unsure
LOCATION: 486, 510, 552, 573
OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.8%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 3.2e-124;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

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DB 1 GGAAGGCGCAATCATCATAGATTAAGAGAGCGGAGAAATTAACAGACAGAACTGAG 60
QY 1681 ACCACAGACATCTCATATATCTCGGTGGGTGCTCAAGGTGAAAACAGTACAGTCC 1740
DB 61 ACCACAGACATCTCATATATCTCGGTGGGTGCTCAAGGTGAAAACAGTACAGTCC 120
QY 1741 ATAGAGTCCAGTGAATGCTGCTTCACTAGACATCTTCAACAGGTCTTGGAAAAGCTCT 1800
DB 121 ATAGAAATCCAAAGCTGAGCTGCTTCACTAGACATCTTCAACAGGTCTTGGAAAAGCTCT 180
QY 1801 GCCTCAGCCCTGCTTGGCTTCACTTCCAGATCCACCTTTGATGTGAAAGACATCT 1860
DB 181 GCCTCAGCCCTGCTTGGCTTCACTTCCAGATCCACCTTTGATGTGAAAGACATCT 240
QY 1861 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1920
DB 241 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 300
QY 1921 TTATCCAGATCACTAGTGGCAATCTCTGAGAGGCTCTGCAATTTCTGAGCCCAAT 1980
DB 301 TTATCCAGATCACTAGTGGCAATCTCTGAGAGGCTCTGCAATTTCTGAGCCCAAT 359
QY 1981 GAGTTGAGTCCAGACTTCTAGCGCTTGAAGCTTACTATGACAGTCAAGCAACAG 2040
DB 360 GAGTTGAGTCCAGACTTCTAGCGCTTGAAGCTTACTATGACAGTCAAGCAACAG 417
QY 2041 GTGCCAATTAAGTCAAGCAAGTGTCTGAGAGGCAAGCAACCAATTTGCAACCA 2100
DB 418 GTGCCAATTAAGTCAAGCAAGTGTCTGAGAGGCAAGCAACCAATTTGCAACCA 475
QY 2101 ATTAATACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2156
DB 476 ATTAATACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 531

RESULT 15
US-09-105-058C-19
Sequence 19, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dwozetzky, Steven
APPLICANT: Gribkooff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubaue, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCMO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105, 058C
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 3287
TYPE: DNA
ORGANISM: Homo sapiens
US-09-105-058C-19

Query Match 15.8%; Score 425; DB 3; Length 3287;

Best Local Similarity 64.7%; Pred. No. 1.3e-115;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

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QY 124 GAGACCCGCGGGGAGAGAGGGGCGCGGATGAGCTCTGCTGGGAAAGCCGCTCTTAC 183
DB 187 GCGGCTCGAGAGCCCGCAAGGGGCGAGCATCTCAGAAACCTCGCGGGGGGGCGG 246
QY 184 ACAGATGACAGAGCTGCGGCGCAAGTCAAGTACCGGCGGTCAGAACTACCTGAC 243
DB 247 GCGGCGGAGAGCCCGCAAGGCGCAACGCTTCTACCCAGAGCTCAGAAATTTCTTAC 306
QY 244 AACGCTGAGAGAGACCCCGGCGGCGTTCATCTCCACAGCTTGTGTTTCTCCTT 303
DB 307 AACGCTGAGAGAGCCCGGCGGCGGCTGAGCTTCACTACAGGCTTACGTTCTCTG 366
QY 304 GCTTGTGGTGTGATTTTGTCAAGTCTTCTACATCTCCAGACACAAATTTGGCC 363
DB 367 GCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
QY 364 TCAAGTGGCTTCTGATCTGAGTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 423
DB 427 GAGGGGGGCTTCTACATCTGGAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
QY 424 ATTCAGATCTGCTGCGGGGCTTGTGCTGATTAAGAGATGAGCAAGAACTGAG 483
DB 487 GTGCGGATCTGAGGCGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
QY 484 TTTGCTGAAAGCCCTTGTGTTTATAGATCAATTTGTTTATGCTTCAATAGCAGTT 543
DB 547 TTTGCTGAAAGCCCTTGTGTTTATAGATCAATTTGTTTATGCTTCAATAGCAGTT 606
QY 544 GTTTTGTCAAAATCTCAGGATTAATTTTGTGCAAGTCTGCACTAGAAATTCCTTTTC 603
DB 607 CTGGCGGCGGCTTCCAGAGGCAAGCTTGTGCAATCTGCTGCTGCTGCTGCTGCTGCT 666
QY 604 CTACAGATCTTCCGATGCTGAGTGAAGCAAGGAGGAGCACTTGAATTAATTCAGG 663
DB 667 CTGCGAGATCTTCCGATGATATCGATGAGACCGGCGGAGGCACTTGAAGTCTGCTG 726
QY 664 TCAAGTGTATAGCTACAGAGAAATTAATCAAGCTTGTATCATAGATTTTGTGTT 723
DB 727 TCTGTGTCTATAGCCCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 724 CTATATTTTGTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
DB 787 CTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 784 ACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 847 ACTTACGCGGATGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
QY 844 AAAATCTCCCTAATCTGCTGAGAGATGCTTCTGCAAGCTTGTGCACTCTTGTGCAAT 903
DB 907 AAGTACCCCAAGACTGAGAGGAGGCTCTTGTGCGCAACTTCACTCATCGGTGTC 966
QY 904 TCTTCTTGTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
DB 967 TCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
QY 964 CAACACGCGCAAAACATTTGAGAAAGAGAAACCCAGCTGCAACTCATTTAGTGT 1023
DB 1027 CAGCAGAGGAGAGCACTTTGAGAAAGAGGCGGAACCGGCAAGAGGCTGATCCAGTCTG 1086
QY 1024 GTTGGCGTGAATTCGC 1040
DB 1087 GCTGAGAGATTTTACGC 1103

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Scoring table: IDENTITY_NUC
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Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 1954462

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2694	100.0	2694	9	US-09-810-796-2
3	2694	100.0	2694	21	US-10-948-493-1
4	2690.4	99.9	3071	9	US-09-810-796-1
5	2689.2	99.8	3137	19	US-10-661-629-1
6	2681.2	99.5	3074	9	US-09-813-148-1
7	2681.2	99.5	3074	21	US-10-399-489A-5

8	2679.6	99.5	3074	21	US-10-482-834A-55	Sequence 55, Appli
9	2630	97.6	2667	9	US-09-810-796-3	Sequence 3, Appli
10	2625.2	97.4	2772	9	US-09-825-147-1	Sequence 1, Appli
11	2625.2	97.4	2772	19	US-10-803-268-1	Sequence 1, Appli
12	2625.2	97.4	3111	9	US-09-825-147-3	Sequence 3, Appli
13	2625.2	97.4	3111	19	US-10-803-268-3	Sequence 3, Appli
14	518.4	19.2	2335	17	US-10-353-650-55	Sequence 55, Appli
15	518.4	19.2	2335	21	US-10-850-928-1	Sequence 1, Appli
16	518.4	19.2	2335	21	US-10-399-489A-4	Sequence 4, Appli
17	516	19.2	2273	16	US-10-096-578-8	Sequence 8, Appli
18	510	18.9	2169	13	US-10-128-870-22	Sequence 22, Appli
19	510	18.9	2169	13	US-10-131-685-22	Sequence 22, Appli
20	509.8	18.9	582	15	US-10-313-542-303	Sequence 303, App
21	500.6	18.6	7407	21	US-10-482-834A-54	Sequence 54, Appli
22	500.6	18.6	7407	21	US-10-482-834A-57	Sequence 57, Appli
23	500.6	18.6	7407	21	US-10-482-834A-58	Sequence 58, Appli
24	500.6	18.6	7407	21	US-10-482-834A-59	Sequence 59, Appli
25	500.6	18.6	7411	20	US-10-335-053-6	Sequence 6, Appli
26	500.6	18.6	7420	17	US-10-295-027-281	Sequence 281, App
27	500.6	18.6	7420	20	US-10-643-795A-75	Sequence 75, Appli
28	500.6	18.6	7420	21	US-10-948-518-75	Sequence 75, Appli
29	500.6	18.6	7420	22	US-10-287-436A-302	Sequence 302, App
30	500.6	18.6	7863	15	US-10-084-817-335	Sequence 335, App
31	499	18.5	7407	21	US-10-482-834A-56	Sequence 56, Appli
32	497.6	18.5	2750	21	US-10-399-489A-2	Sequence 2, Appli
33	480.6	17.8	7413	22	US-10-450-763-10636	Sequence 10636, A
34	478.4	17.8	5595	19	US-10-820-307-8	Sequence 8, Appli
35	477	17.7	3195	22	US-10-450-763-10635	Sequence 10635, A
36	465.8	17.3	2766	13	US-10-820-307-6	Sequence 6, Appli
37	465.4	17.3	896	14	US-10-128-870-1	Sequence 1, Appli
38	465.4	17.3	896	14	US-10-131-685-1	Sequence 1, Appli
39	465	17.3	548	16	US-09-826-724-269	Sequence 269, App
40	464	17.2	2814	16	US-10-096-578-90	Sequence 90, Appli
41	460.8	17.1	2665	13	US-10-128-870-26	Sequence 26, Appli
42	460.8	17.1	2665	13	US-10-131-685-26	Sequence 26, Appli
43	460.8	17.1	2914	16	US-10-096-578-6	Sequence 6, Appli
44	460.8	17.1	2926	21	US-10-482-834A-53	Sequence 53, Appli
45	460.8	17.1	2926	21	US-10-482-834A-61	Sequence 61, Appli

ALIGNMENTS

RESULT 1
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1621 GGAAGAGGGCAAAATACATCAGATAGAGAGCGGAGAAATTAACAGCAAGAAATAG 1680
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Qy 1681 ACCACAGACATCTCAGATGCTCGGTGGGTGCTCAAGTTGAAAAACAGTACAGTCC 1740
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Qy 1801 GCTTCAGCCCTCGCTTGGCTTCAATCCAGATCCACCTTTTGAATGGAACAGACATCT 1860
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Db 1861 GACTATCAAAAGCCCTGTGATGAGCAAGATCTTTCGAGTTCGCGCAAAAAGTGGCTGC 1920
Qy 1921 TTATCAGATCAACTAGTGCACAATCTCGAAGGCTTCGAGTTCAATTTCTGACGCCAAT 1980
Db 1921 TTATCAGATCAACTAGTGCACAATCTCGAAGGCTTCGAGTTCAATTTCTGACGCCAAT 1980
Qy 1981 GAGTTCAATGCGCAGACTTCTTACGCGGTTAGCCCTATATGACAGTCAAGCAACAGAG 2040
Db 1981 GAGTTCAATGCGCAGACTTCTTACGCGGTTAGCCCTATATGACAGTCAAGCAACAGAG 2040
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QY	2281	TCAAAATCTCACCAAGGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGAGAAACTCTG	2340
Dp	2281	TCAAAATCTCACCAAGGACCGTTCTATGAGAAAAAGCTTTGACATGGAGGAGAAACTCTG	2340
QY	2341	TTGTCTGTCTGTCCATGCTGTCGCGAAGACCTTGGCAATCTTTGTCTGTGCAAAACCTG	2400
Dp	2341	TTGTCTGTCTGTCCATGCTGTCGCGAAGACCTTGGCAATCTTTGTCTGTGCAAAACCTG	2400
QY	2401	ATCAGGTGACCCGAGAACGTGAATTAACACTTTTCAGGAGTGAAGTCAAGTGCTCCAGA	2460
Dp	2401	ATCAGGTGACCCGAGAACGTGAATTAACACTTTTCAGGAGTGAAGTCAAGTGCTCCAGA	2460
QY	2461	GGCAGCCAAATTTTATCCCAAAATGAGGGAATCCAAATTTGTTATTACTGATGAAGAG	2520
Dp	2461	GGCAGCCAAATTTTATCCCAAAATGAGGGAATCCAAATTTGTTATTACTGATGAAGAG	2520
QY	2521	GTCGGTCCCGAAGACAGACAGACACTTTTATGTCGCGACCGGACCTGCCAGGAA	2580
Dp	2521	GTCGGTCCCGAAGACAGACAGACACTTTTATGTCGCGACCGGACCTGCCAGGAA	2580
QY	2581	GCTGCTTTGGCATCAGACTCTCTAAGACTGGAAGTTCACGATCATCTCAGAGCAATTTGT	2640
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QY	2641	AAAGCAGGAAGAAAGTACAGATGCTCTCAGCTTTCCTCATGTCAAACTGAATAA	2694
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RESULT 2
US-09-810-796-2
? Sequence 2, Application US/09810796
? Patent No. US20020102677A1
? GENERAL INFORMATION:
? APPLICANT: Jegia, Timothy James
? APPLICANT: ICAGEN, Inc.
? TITLE OF INVENTION: KCNO5, a NO
? FILE REFERENCE: 018512-005010US
? CURRENT APPLICATION NUMBER: US/09/810, 796
? CURRENT FILING DATE: 2001-10-12
? PRIOR APPLICATION NUMBER: US 60/190,954
? PRIOR FILING DATE: 2000-03-21
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2
? LENGTH: 2694
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: human outwardly-rectifying, voltage-gated
? OTHER INFORMATION: potassium channel KCNO5-1 coding sequence
? NAME/KEY: CDS
? LOCATION: (1)..(2694)
? OTHER INFORMATION: KCNO5-1
? US-09-810-796-2

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Query Match	100.0%	Score 2694	DB 9	Length 2694
Best Local Similarity	100.0%	Pred. No. 0		
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Db 1 ATGAAGATGTGAGATCGGGGCCGGGGGCAAGGGTCTGCTGAACCTGGCAGCCGCCAGGGGGC 60
QY 61 GACGGCCTGTACTGCTGGGACCCGCGCGGACAGCTTGATGGCGGCGGGTGGCTTG 120
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QY	241	TACAAAGTGCAGAGAGACCCCGCGGGCGGGGGTTCACTCAACAGCTTGGTTTTCTC	300
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QY	301	CTTGTCTTGGTGGCTGATTTTGTCACTGTTTCTACACTCCCTGAGACACAAATTG	360
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QY 1921 TTATCCAGATCACTAGTGCACAACTCTGAGAGGCTGCAAGTCAATCTGACGCCAAT 1980
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RESULT 3
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US2005006491A1
; GENERAL INFORMATION:
; APPLICANT: DWOIRETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCMOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 100.0%; Score 2694; DB 21; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTTCGCGCCGCGGCGAGGCTGCTGAACTCGGACGCGCGAGGCG 60
Db 1 ATGAAGATGTGAGTTCGCGCCGCGGCGAGGCTGCTGAACTCGGACGCGCGAGGCG 60
QY 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCACAGCTTGTGTGGGCGGCGGTGGCTG 120
Db 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCACAGCTTGTGTGGGCGGCGGTGGCTG 120
QY 121 AGGAGAGCCGCGGCGGCAAGAGGAGGCGCGGATGAGCTGCTGGGGAAGCGGCTCT 180
Db 121 AGGAGAGCCGCGGCGGCAAGAGGAGGCGCGGATGAGCTGCTGGGGAAGCGGCTCT 180
QY 181 TACAGAGTATGACAGAGTTCGCGGCGCAACGTCAAGTACCGCGGCTGCAAGTACCTG 240
Db 181 TACAGAGTATGACAGAGTTCGCGGCGCAACGTCAAGTACCGCGGCTGCAAGTACCTG 240
QY 241 TACAACTGCTGAGAGACCCCGCGGCTGGCGTTCACTACACGCTTTGCTTTCTC 300
Db 241 TACAACTGCTGAGAGACCCCGCGGCTGGCGTTCACTACACGCTTTGCTTTCTC 300

Db 241 TACAGTGTGAGAGACCCCGGCGTGGCGTCACTACACAGCTTTCGTTTTC 300
Qy 301 CTGTCTTTGGTGTCTGATTTTGTCACTGTTTTCACATCCCTGAGCACAAAATTG 360
Db 301 CTGTCTTTGGTGTCTGATTTTGTCACTGTTTTCACATCCCTGAGCACAAAATTG 360
Qy 361 GCGTCAGTGGCCTTGATCTGGAGTGTGATGATGCTGCTTGGTTGGAGTTC 420
Db 361 GCGTCAGTGGCCTTGATCTGGAGTGTGATGATGCTGCTTGGTTGGAGTTC 420
Qy 421 ATCATTCGAATCTGTGTGCGGGTGTCTGTGTGATATAGAGATGCGAAGAACTG 480
Db 421 ATCATTCGAATCTGTGTGCGGGTGTCTGTGTGATATAGAGATGCGAAGAACTG 480
Qy 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGCTTACCAATAGCA 540
Db 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGCTTACCAATAGCA 540
Qy 541 GTTGTTCGCAAAAACCTCAGGGTAATTTTGGCAGCTGCACTCAGAGTCCGT 600
Db 541 GTTGTTCGCAAAAACCTCAGGGTAATTTTGGCAGCTGCACTCAGAGTCCGT 600
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Db 601 TTCTCAGATCTCCGATGTGTGCGCATGACGGAAGGAGGCACTTGGAAATTA 660
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Db 961 GAACAACACCGCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGCAACTATTGAG 1020
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Db 1081 CACTTAAAGGCTTTCACACCTGACGCTTCAAGAAATCTGTTTCAATTCACCTTGAAGCCA 1140
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Db 1141 AGTCAGAAAGCTTTTAAAGAGCAGTGTGCGATGGCTAGCCCAAGGGGCTCAGATATT 1200
Qy 1201 AAGAGCCGACAGCTTCAGTGTGACAGAGGTCCCAAGACACGATCAGACCGGAG 1260
Db 1201 AAGAGCCGACAGCTTCAGTGTGACAGAGGTCCCAAGACACGATCAGACCGGAG 1260
Qy 1261 GGGAGTCCCAAGAGGAGAGAGAGTGTGAGCTTCAAGACCGGCTTCCGAGCC 1320
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Db 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTGTATAGTCTGACAGCCCTTGGC 1380

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Qy 1381 ACTGATGATGTATATATATGAAAAAGATGCGCAGTGTGATGTATCAGTGGAAAGCCTCAC 1440
Db 1381 ACTGATGATGTATATATATGAAAAAGATGCGCAGTGTGATGTATCAGTGGAAAGCCTCAC 1440
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Db 1741 ATAGAGTCCAAAGTGTGATGCTCTATAGCATCTATCAACAGTCTTGGGAAAGGCTCT 1800
Qy 1801 GCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTGAAATGTGAACAGACATCT 1860
Db 1801 GCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTGAAATGTGAACAGACATCT 1860
Qy 1861 GACTATCAAGCCCTGTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGTGTGC 1920
Db 1861 GACTATCAAGCCCTGTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGTGTGC 1920
Qy 1921 TTAATCAGATCAATATATGTGCAACATCTGAGAGGCTGCAATTTCTGACGCCAAT 1980
Db 1921 TTAATCAGATCAATATATGTGCAACATCTGAGAGGCTGCAATTTCTGACGCCAAT 1980
Qy 1981 GAGTTGAGGCCCAAGCTTTCAGCGGCTTACGCCCTATGACAGTCAAGTCAAGCACAG 2040
Db 1981 GAGTTGAGGCCCAAGCTTTCAGCGGCTTTCAGCGGCTTACGCCCTATGACAGTCAAGTCAAGCACAG 2040
Qy 2041 GTGCAATTAATGTCAAAGCGATGCTCAGCAGTGTGAGCAGCAGCAACATTCGAAACCA 2100
Db 2041 GTGCAATTAATGTCAAAGCGATGCTCAGCAGTGTGAGCAGCAGCAACATTCGAAACCA 2100
Qy 2101 ATTAATACGGACCCAGCAGAGGCCCAACATCTTACAGATCCACCTCTCCCA 2160
Db 2101 ATTAATACGGACCCAGCAGAGGCCCAACATCTTACAGATCCACCTCTCCCA 2160
Qy 2161 GCATCAAGCATCTGCGCAGGCAAGAACTGCAACCCCTCAAGCTTCAAGGAA 2220
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QY 2461 GGCAGCCAAAGATTTTACCCTAATGAGGGAATCCAAATTGTTTAACTGATGAAG 2520
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QY 2521 GTGGGTCCTCCGAGAGACAGAGACACACTTTTGTATGCGCAGCCGCTCCGAGGAA 2580
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DB 2641 AAGGCAAGAAAGTACAGATGCTCCTCAGCTTGCCTCATCTCAAACTGAATA 2694

RESULT 4
US-09-810-796-1
; Sequence 1, Application us/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jogle, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCON5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: us/09/810, 796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCON5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCON5-1
US-09-810-796-1

Query Match 99.9%; Score 2690.4; DB 9; Length 3071;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTCGGGCGGAGGCAAGGTCGTGTAACCTCGGACGCGCAAGGAGC 60
DB 10 ATGAAGATGTGAGTCGGGCGGAGGCAAGGTCGTGTAACCTCGGACGCGCAAGGAGC 69
QY 61 GACGCGCTCTACTGCTGGGACACCGCGCGGCAACGCTTGTGTGGCGGCGGCTGCTG 120
DB 70 GACGCGCTCTACTGCTGGGACACCGCGCGGCAACGCTTGTGTGGCGGCGGCTGCTG 129
QY 121 AAGGAGAGCGCGCGGAGCAAGCAAGGAGGCGCGGATGAGCTGTGGGAAAGCGCTCTCT 180
DB 130 AAGGAGAGCGCGCGGAGCAAGCAAGGAGGCGCGGATGAGCTGTGGGAAAGCGCTCTCT 189
QY 181 TACACAGATGACCAAGCTGCGGCGCAACGTCMAATACCGGCGGCTGCAAGACTACCTG 240
DB 190 TACACAGATGACCAAGCTGCGGCGCAACGTCMAATACCGGCGGCTGCAAGACTACCTG 249
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DB 250 TACAAAGCTGTGAGAGACACCGCGGCTGGGCTTATCTACACGCTTTGTTTTCTC 309
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DB 370 GCTTCAGATTGCTCTTGATCTCGAGTTCGTGATGATTTGTCGTTGTTGGATTTC 429
QY 421 ATCATTCGAATCTGGTCTGCGGCTTGTGCTGATATAGAGATGCGCAAGAAAGCTG 480
DB 430 ATCATTCGAATCTGGTCTGCGGCTTGTGCTGATATAGAGATGCGCAAGAAAGCTG 489
QY 481 AGGTTGCTCGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
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QY 1261 GGCAGTCCCAAAAGTTCACGCAAAACAGAGTATGCTGACACAGCCCTTGGGC 1320
DB 1270 GGCAGTCCCAAAAGTTCACGCAAAACAGAGTATGCTGACACAGCCCTTGGGC 1329
QY 1321 TCGTGTGCTCCAAAGTTCTCAGCCCAAAACAGAGTATGCTGACACAGCCCTTGGGC 1380
DB 1330 TCGTGTGCTCCAAAGTTCTCAGCCCAAAACAGAGTATGCTGACACAGCCCTTGGGC 1389
QY 1381 ACTGATGATGATATGATGAAAGAGATGCAAGTGTGATGATCAGTGAAGACCTTACC 1440
DB 1390 ACTGATGATGATATGATGAAAGAGATGCAAGTGTGATGATCAGTGAAGACCTTACC 1449
QY 1441 CCACCCTTAAACCTGATTCAGAGCTATACGAATATGAAATTTTCATGTTGCAAAACGG 1500

Db 1450 CCACCACTTAACTGTCATTCAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1509
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QY 1621 GGAAGAGGCAATTCATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAAACTAG 1680
Db 1630 GGAAGAGGCAATTCATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAAACTAG 1689
QY 1681 ACCACAGACATCTCAGATAGCTCGCTGCGGTGCTCAAGGTTGAAAAACGATACGCTC 1740
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Db 1750 ATAGAGTCCAGGTGAGTGCCTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCT 1809
QY 1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1810 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1869
QY 1861 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTCCGGGTCCGACAAAAAGTGGCTGC 1920
Db 1870 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTCCGGGTCCGACAAAAAGTGGCTGC 1929
QY 1921 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTGAGGTTCAATTCAGACGCAAAAT 1980
Db 1930 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTGAGGTTCAATTCAGACGCAAAAT 1989
QY 1981 GAGTCAAGTCCAGACCTTTCTACGGCTTACGCTTACCTAATGACAGTCAAGCAACAG 2040
Db 1990 GAGTCAAGTCCAGACCTTTCTACGGCTTACGCTTACCTAATGACAGTCAAGCAACAG 2049
QY 2041 GTGCCAATTAAGTCAAAAGCGATGCTCAGCAGTGGCAGCCCAACACATTTGCAAAACCA 2100
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QY 2101 ATAAATACGGGACCCCAAGGACGAGCCCAACAACTTTACATGATCCCACTCTCTCCCA 2160
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QY 2161 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGCAACCTTAACCTGAGGCTTACAGAA 2220
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QY 2281 TCAAACTCAACCAAGGACGTTCTATGAGGAAAGCTTGAACATGGGAGGAGAACTCTG 2340
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QY 2401 ATCAGGTCGACGAGGAACTGAATATACAACTTTCAAGGAGTGAATCAAGTGGCTCCAG 2460
Db 2410 ATCAGGTCGACGAGGAACTGAATATACAACTTTCAAGGAGTGAATCAAGTGGCTCCAG 2469
QY 2461 GGCAGCCAAATTTTAAACCCCAATGAGGGAATCCAAATTTGTTTAACTGAAGAG 2520
Db 2470 GGCAGCCAAATTTTAAACCCCAATGAGGGAATCCAAATTTGTTTAACTGAAGAG 2529
QY 2521 GTGGGTCCTCCAGAGACAGAGACACTTTTGAATGCGCACGCAAGCTGCGAGGGA 2580

Db 2530 GTGGGTCCTCCAGAGACAGACAGACACTTTTGAATGCCGACCGGAGCTCCAGGGA 2589
QY 2581 GGTGCTTTGATCAGACTCTGTAAGACTGGAAGGTGACATCATCTCAGACATTTGT 2640
Db 2590 GGTGCTTTGATCAGACTCTGTAAGACTGGAAGGTGACATCATCTCAGACATTTGT 2649
QY 2641 AAGGACGAGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2694
Db 2650 AAGGACGAGAAAGTACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA 2703

RESULT 5
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
; FILE REFERENCES: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Query Match 99.8%; Score 2689.2; DB 19; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTCCGGGCGGAGGAGGCTGCTGAACTCGGCAAGCCGCGAGGCG 60
Db 1 ATGAAGATGTGAGTCCGGGCGGAGGAGGCTGCTGAACTCGGCAAGCCGCGAGGCG 60
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Db 61 GACGCGCTGCTACTGCTGCGGACCCGCGCGCACGCTCGTGGCGGCGGCTGCTG 120
QY 121 AAGGAGAGCGCGCGGAGGAGGAGGCGCGGATGAGCTGCTGGGGAAGCGGCTCT 180
Db 121 AAGGAGAGCGCGCGGAGGAGGAGGCGCGGATGAGCTGCTGGGGAAGCGGCTCT 180
QY 181 TACACGATGAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGAGTGAAGACTAC 240
Db 181 TACACGATGAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGAGTGAAGACTAC 240
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Db 301 CTGTGCTTGTGCTGATATTTTGTGACAGTCTTCTACATCCCTGAGACACAAATG 360
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QY 421 ATCATTCGAATCTGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 ATCATTCGAATCTGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Db 481 AGGTTTGTCTGGAAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GTTGTCTGCAAAAACTCAGGATTAATTTTGGCAGCTGCACTCAGAAAGTCTCGT 600

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Db 541 GTGTGTTTCGCAAAAACCTCAGGGGTATATTTTTCACAGCTGCACTCAGAAAGTCTCCGT 600
QY 601 TTCCTACAGATCCCTCGGANTGTCGCGCATGAGACCGAAGGGGAGGCACTTGAAATTAACG 660
Db 601 TTCTTACAGATCCCTCGGANTGTCGCGCATGAGACCGAAGGGGAGGCACTTGAAATTAACG 660
QY 661 GGTTTCAGTGGTTTATGCTCAGACAGAAAGATTATCAGAGCTTGATGACATAGGATTTTG 720
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Db 901 ATTTCTTTCTTTGCACTTCTGCGCATTTCTTGCTCAGGTTTTCATTAAAGTACAA 960
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QY 1201 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGGTGCCCAAGCACCGACATCAAGCCGAG 1260
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Db 1321 TCGCTGCGGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGACACAGCCCTTGGC 1380
QY 1381 ACTGATGATGATATGATGAAAAAGATCCAGTGTGATGATCACTGAGAGACCTCAC 1440
Db 1381 ACTGATGATGATATGATGAAAAAGATCCAGTGTGATGATCACTGAGAGACCTCAC 1440
QY 1441 CACACACTTAAACCTGCTATGAGCTATCAGAAATTAAGAAATTTCAATGTCAAAACG 1500
Db 1441 CACACACTTAAACCTGCTATGAGCTATCAGAAATTAAGAAATTTCAATGTCAAAACG 1500
QY 1501 AAGTTTAAAGAAAGTTACGTCATGATGATTAAGATGTCATTGAAACATATTCTGCT 1560
Db 1501 AAGTTTAAAGAAAGTTACGTCATGATGATTAAGATGTCATTGAAACATATTCTGCT 1560
QY 1561 GGTCACTGTGACATGTTGTGTAAGATTAAAGCCTTCAACAAGTGTGATCAAAATTTCT 1620
Db 1561 GGTCACTGTGACATGTTGTGTAAGATTAAAGCCTTCAACAAGTGTGATCAAAATTTCT 1620
QY 1621 GGAAGAGGCAATCATCATATGAGAGCGGAGAGAAATTAACAGACAGACATGAG 1680
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Db 1621 GGAAGAGGCAATCATCATATGAGAGCGGAGAGAAATTAACAGACAGACATGAG 1680
QY 1681 ACCACAGACGATCTAGATGCTGCTGCGGAGTGCAGAGTTGAAAAACAGGTACAGTCC 1740
Db 1681 ACCACAGACGATCTAGATGCTGCTGCGGAGTGCAGAGTTGAAAAACAGGTACAGTCC 1740
QY 1741 ATGAGTCCAAAGCTGACCTGCTACTAGACATCTATCAACAGGTCTCTCGAAAAGCTCT 1800
Db 1741 ATGAGTCCAAAGCTGACCTGCTACTAGACATCTATCAACAGGTCTCTCGAAAAGCTCT 1800
QY 1801 GCTCAGCCCTGCTTGGCTTCACTTCAGATCCCACTTTTGAATGTAACAGCATCT 1860
Db 1801 GCTCAGCCCTGCTTGGCTTCACTTCAGATCCCACTTTTGAATGTAACAGCATCT 1860
QY 1861 GACATCAAGAGCCCTGATAGCAAAAGATCTTTCAGGTCGCGCAAAAAGTGGCTGC 1920
Db 1861 GACATCAAGAGCCCTGATAGCAAAAGATCTTTCAGGTCGCGCAAAAAGTGGCTGC 1920
QY 1921 TTATCAGATCAACTAGTCCCAACATCTGAGAGGCTGCAAGTTGATTCGACGCAAT 1980
Db 1921 TTATCAGATCAACTAGTCCCAACATCTGAGAGGCTGCAAGTTGATTCGACGCAAT 1980
QY 1981 GAGTTCAAGTCCCAAGCTTCTGAGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
Db 1981 GAGTTCAAGTCCCAAGCTTCTGAGCGCTTACGCTTACTATGACAGTCAAGCAACAG 2040
QY 2041 GTGCCAATTAAGTCAAAAGGATGGCTCAGCAGTGGAGGCAACACACATTGCAAAACCA 2100
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QY 2101 ATAAATACGGGACCCCAAGCCAGAGCCGCCCAACATTTTACAGATCCACTCTCTCCA 2160
Db 2101 ATAAATACGGGACCCCAAGCCAGAGCCGCCCAACATTTTACAGATCCACTCTCTCCA 2160
QY 2161 GGCATCAAGCATGTCGCCCAAGGCGCAAGAACTGTGACCCCTTAACTCTGACAGCTTACAGAA 2220
Db 2161 GGCATCAAGCATGTCGCCCAAGGCGCAAGAACTGTGACCCCTTAACTCTGACAGCTTACAGAA 2220
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QY 2401 ATCAGGTGACCGAGAACTGAATATACAACTTTCAGAGGAGTGAAGTCAAGTGCCTCAGA 2460
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QY 2461 GGCAGCCAAATTTTACCCCAATGAGGGAATCCAAATGTTTATTAACGTATGAAG 2520
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Db 2521 GTGGGTCCCGAAGAGACAGACAGACACTTTGATGCGGACCGAGACCTGCCAGGGAA 2580
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Db 2581 GCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGGTACAGATCATCTCAGAGCATTTGT 2640
QY 2641 AAGCAGAGAAAGTACAGATGCTCCTCAGCTTGCTCATGTCAAACTGAATTA 2694
Db 2641 AAGCAGAGAAAGTACAGATGCTCCTCAGCTTGCTCATGTCAAACTGAATTA 2694

RESULT 6
US-09-813-148-1

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Sequence 1, Application US/09813148
Patent No. US20020076809A1
GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERSCHE, Christlan
APPLICANT: SCHERER, Constanze
APPLICANT: SEESOHM, Giselcard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

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Db 1955 ATGAAATCCAAAGTGAAGTGGCTGCTTACATGACATCTATCAACAGTCTCTTGGAAGGCTCT 2014
QY 1801 GCCTCAAGCCCTGCTTGGCTTATTCAGATCCACCTTTGATGTAAGACATCT 1860
Db 2015 GCTTCAGCCCTGCTTGGCTTATTCAGATCCACCTTTGATGTAAGACATCT 2074
QY 1861 GACTATCAAGCCCTGCTTGGCTTATTCAGATCCACCTTTGATGTAAGACATCT 1920
Db 2075 GACTATCAAGCCCTGCTTGGCTTATTCAGATCCACCTTTGATGTAAGACATCT 2134
QY 1921 TTAATCAAGATCACTGATGCAATCTGAGAGGCTGCAATCTTGAAGCCCAAT 1980
Db 2135 TTAATCAAGATCACTGATGCAATCTGAGAGGCTGCAATCTTGAAGCCCAAT 2194
QY 1981 GAGTTGAGTCCAGAGCTTCTGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2040
Db 2195 GAGTTGAGTCCAGAGCTTCTGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2254
QY 2041 GTGCAATTAATGTCAAAGCATGCTGAGAGTGGAGCCCAACCAATTCGAAACCA 2100
Db 2255 GTGCAATTAATGTCAAAGCATGCTGAGAGTGGAGCCCAACCAATTCGAAACCA 2314
QY 2101 ATAAATACGAGCCCAAGCATGCTGAGAGTGGAGCCCAACCAATTCGAAACCA 2160
Db 2315 ATAAATACGAGCCCAAGCATGCTGAGAGTGGAGCCCAACCAATTCGAAACCA 2374
QY 2161 GGCATCAAGCATGCTGAGAGTGGAGCCCAACCAATTCGAAACCA 2220
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QY 2221 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCAAGAGAAATGTTGAGTTCAG 2280
Db 2435 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCAAGAGAAATGTTGAGTTCAG 2494
QY 2281 TCMAATCTCAACCAAGGCTTCTATGAGAGAAAGTTTGAATGAGAGAGAACTCTG 2340
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QY 2341 TTGTCTGTCTGCTTCCATGCTGAGAGAACTTGTGCTGCTGCAAACTCTG 2400
Db 2555 TTGTCTGTCTGCTTCCATGCTGAGAGAACTTGTGCTGCTGCAAACTCTG 2614
QY 2401 ATCAGTTCAGACGAGAACTGAATATATCACTTTCAGAGAGTGAAGTTCAGAG 2460
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QY 2461 GGCAGCCAGATTTTAACTTCAATGAGAGAACTTTCATGATGAGAG 2520
Db 2675 GGCAGCCAGATTTTAACTTCAATGAGAGAACTTTCATGATGAGAG 2734
QY 2521 GTGGGTCCGAGAGACAGACAGACTTTTGTATGCTGAGAGCTGCTGAGAG 2580
Db 2735 GTGGGTCCGAGAGACAGACAGACTTTTGTATGCTGAGAGCTGCTGAGAG 2794
QY 2581 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAATCTGAGAGATTTGT 2640
Db 2795 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAATCTGAGAGATTTGT 2854
QY 2641 AAGGCAAGAGAAATGATGATGCTGAGAGTGAAGTCAATCTGAGAGATTTGT 2694
Db 2855 AAGGCAAGAGAAATGATGATGCTGAGAGTGAAGTCAATCTGAGAGATTTGT 2908

RESULT 7

US-10-399-489A-5
; Sequence 5, Application US/10399489A
; Publication No. US20050101004A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: ARGENTIERI, Thomas M.
; APPLICANT: SHELDON, Jeffrey H.
; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION

FILE REFERENCE: AM100620
; CURRENT APPLICATION NUMBER: US/10/399,489A
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/241,078
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/US01/32371
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/281,428
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-489A-5

Query Match 99.5%; Score 2681.2; DB 21; Length 3074;

Best Local Similarity 99.7%; Pred. No. 0; Mismatches 8; Indels 0; Gaps 0;

Matches 2686; Conserved 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAAAGATGAGAGTGGAGGCGAGGAGTGTGTAAGTGGAGCGGCGAGGCG 60
Db 215 ATGAAAGATGAGAGTGGAGGCGAGGAGTGTGTAAGTGGAGCGGCGAGGCG 274
QY 61 GACGCGCTGCTAATGCTGAGGAGCCCGCGGCAAGCTTGTGAGGCGGCGGCTG 120
Db 275 GACGCGCTGCTAATGCTGAGGAGCCCGCGGCAAGCTTGTGAGGCGGCGGCTG 334
QY 121 AGGAGAGCCCGCGGAGCAAGGAGGCGCGGAGTGAAGCTGCTGCTCT 180
Db 335 AGGAGAGCCCGCGGAGCAAGGAGGCGCGGAGTGAAGCTGCTGCTCT 394
QY 181 TACAGAGTGAAGAGAGTGGCGGCGCAAGCTCAAGTCCGCGGAGTCAAGTCTG 240
Db 395 TACAGAGTGAAGAGAGTGGCGGCGCAAGCTCAAGTCCGCGGAGTCAAGTCTG 454
QY 241 TACAAAGTGTGAGAGAGCCCGCGGCTGAGCTTCAATCAAGCTTGTCTCTC 300
Db 455 TACAAAGTGTGAGAGAGCCCGCGGCTGAGCTTCAATCAAGCTTGTCTCTC 514
QY 301 CTGTCTTGTGCTTGTATTTGTGATGCTTCTACCAATCCCTGAGACACAAATTTG 360
Db 515 CTGTCTTGTGCTTGTATTTGTGATGCTTCTACCAATCCCTGAGACACAAATTTG 574
QY 361 GCTCAAGTGTGCTTGTATTTGTGATGCTTCTACCAATCCCTGAGACACAAATTTG 420
Db 575 GCTCAAGTGTGCTTGTATTTGTGATGCTTCTACCAATCCCTGAGACACAAATTTG 634
QY 421 ATCAATCGAATCTGATCTGAGGCTTGTGATGCTTGTGATGAGAGTGAAGTCTG 480
Db 635 ATCAATCGAATCTGATCTGAGGCTTGTGATGCTTGTGATGAGAGTGAAGTCTG 694
QY 481 AGTTTGTCTGAAAGCCCTTCTGTTTATGATATCAATCTTCTTATGCTTCAATGAC 540
Db 695 AGTTTGTCTGAAAGCCCTTCTGTTTATGATATCAATCTTCTTATGCTTCAATGAC 754
QY 541 GTTGTCTGCAAAAGTCAAGGTAATTTTGTGCAAGTCTGCAAGTCTGCTGCT 600
Db 755 GTTGTCTGCAAAAGTCAAGGTAATTTTGTGCAAGTCTGCAAGTCTGCTGCTGCT 814
QY 601 TTCTACAGATCTTCCGATGCTGAGAGTGAAGGAGGAGCACTTGAATAATGAC 660
Db 815 TTCTACAGATCTTCCGATGCTGAGAGTGAAGGAGGAGCACTTGAATAATGAC 874
QY 661 GCTTCAGTGTGTTATGCTACAGAGAAATTAATCAAGTCTGCTGATGATGATTTTG 720
Db 875 GCTTCAGTGTGTTATGCTACAGAGAAATTAATCAAGTCTGCTGATGATGATTTTG 934
QY 721 GTTCTATTTTGTGCTTCTGCTTGTATGCTGAGAGAGAGTGAAGTGAAGTGT 780
Db 935 GTTCTATTTTGTGCTTCTGCTTGTATGCTGAGAGAGAGTGAAGTGAAGTGT 994

QY	781	TCATCATATGAGATAGCTCTCGAGGGGACCAATTACATTTAGCAACATTTGGCTATGGA	840
Db	995	TCTACATATGACAGATGCTCTCTGGTGGGGACAAATTACATTTGACACTATTTGGCTATGGA	1054
QY	841	GACAAACATCCCTTAACCTTGGCTGGGAAGATTCTTCTGACAGCTTTGCACTCCCTGGC	900
Db	1055	GACAAACATCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGACAGGCTTTGCACTCCCTGGC	1114
QY	901	ATTTCTTTCTTTTGCACTTCCTGCGGCAATCTTGGCTCAGGTTTTTGCAATTAAGTACA	960
Db	1115	ATTTCTTTCTTTTGCACTTCCTGCGGCAATCTTGGCTCAGGTTTTTGCAATTAAGTACA	1174
QY	961	GACACACACCGCGAGAAAACATTTAGAAAAAGAGAAACCAAGCTGCCAATCTCATAG	1020
Db	1175	GACACACACCGCGAGAAAACATTTAGAAAAAGAGAAACCAAGCTGCCAATCTCATAG	1234
QY	1021	TGTGTTTGGCTAGTTAGCGACGCTGATGAGAAATCTGTTCCATTTGCAACTGGAAGCCA	1080
Db	1235	TGTGTTTGGCGTAGTTAGCGACGCTGATGAGAAATCTGTTCCATTTGCAACTGGAAGCCA	1294
QY	1081	CACTTGAAAGCCTTGACACCTGCGACCCCTTACCAAGAAAGAACAAAGGGAAAGCATCAAGC	1140
Db	1295	CACTTGAAAGCCTTGACACCTGCGACCCCTTACCAAGAAAGAACAAAGGGAAAGCATCAAGC	1354
QY	1141	AGTCAGAAAGCTAAGTTTTAAGGAGGAGTGGGCAATGGCTACGCCAGGGGGCAGAGATT	1200
Db	1355	AGTCAGAAAGCTAAGTTTTAAGGAGGAGTGGGCAATGGCTACGCCAGGGGGCAGAGATT	1414
QY	1201	AAGAGCCGACAAGCCTCAGTAGTGACAAGAGAGTCCCAACACCCGACATCACAGCCGAG	1268
Db	1415	AAGAGCCGACAAGCCTCAGTAGTGACAAGAGAGTCCCAACACCCGACATCACAGCCGAG	1474
QY	1261	GGCAGTCCCAACAAAGTGCAAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCGAGCC	1320
Db	1475	GGCAGTCCCAACAAAGTGCAAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCGAGCC	1534
QY	1321	TTCGCTGGCCCTCCAAAAGTTCTCAGCCAAACACAGTAGTAGTGCATGACACAGCCCTTGGC	1380
Db	1535	TTCGCTGGCCCTCCAAAAGTTCTCAGCCAAACACAGTAGTAGTGCATGACACAGCCCTTGGC	1594
QY	1381	ACTGATGATGTATATGATGAAGAAAAGGATGCGAGTGTGATGATCAGTGGGAAGACCTCAC	1440
Db	1595	ACTGATGATGTATATGATGAAGAAAAGGATGCGAGTGTGATGATCAGTGGGAAGACCTCAC	1654
QY	1441	CCACCACTTAAACCTGCTATTGAGCTATCAGAAATTATGAATTTCAATGTTGCCAAAACGG	1500
Db	1655	CCACCACTTAAACCTGCTATTGAGCTATCAGAAATTATGAATTTCAATGTTGCCAAAACGG	1714
QY	1501	AAGTTTAAGGAAAGCTTACGTCATATGATGTAATAAAGTGTCAATTTGCAATATTTGCT	1560
Db	1715	AAGTTTAAGGAAAGCTTACGTCATATGATGTAATAAAGTGTCAATTTGCAATATTTGCT	1774
QY	1561	GGTCATCTGACATGTTGTGTAGAAATTAAAGCCTTCAACACGCTTGATCAAAATGCTT	1620
Db	1775	GGTCATCTGACATGTTGTGTAGAAATTAAAGCCTTCAACACGCTTGATCAAAATGCTT	1834
QY	1621	GGAAGAGGCAATACATCATAGATPAGAGAGCGGAGAGAAATPACAGCAATATGAG	1680
Db	1835	GGAAGAGGCAATACATCATAGATPAGAGAGCGGAGAGAAATPACAGCAATATGAG	1894
QY	1681	ACCAACAGACATCTCAGTAGTGTGCTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1740
Db	1895	ACCAACAGACATCTCAGTAGTGTGCTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1954
QY	1741	ATTAGAGTCCAAGCTGGGACCTGCTCTACATCTATCAACATGACAGGTCTTCGGAAAGGCTCT	1800
Db	1955	ATTAGAGTCCAAGCTGGGACCTGCTCTACATCTATCAACATGACAGGTCTTCGGAAAGGCTCT	2014
QY	1801	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGGAACAGACATCT	1860
Db	2015	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGGAACAGACATCT	2074
QY	1861	GACTATCAAAAGCCCTGTGTGATAGCAAGATCTTTGGGTTCCGACAAACACATGTGGCTGC	1920

Db	2075	GACATATAAGCCCTGTGATAGGAAGAATCTTTCCGGTTCCCGACAAACATGGCTGC	2134
Qy	1921	TTATCCAGATCACTAGTGCACAATCTCGAAGGCGCTGCAGTTCAATCTGAGGCCAAT	1980
Db	2135	TTATCCAGATCAACTGTGCGCAACATCTCGAGAGGCGCTGCAGTTCAATCTGAGGCCAAT	2194
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Db	2195	GAGTTCAGTCCCGCAGACTTTCTACGCGCTTAAGCCCTAATAAGACAGTCAAGAACACAG	2254
Qy	2041	GTCGCAATTAGTCAAAAGCGATGGCTCGAGCTGGAGCCCAACAACATTTGCAAAACCA	2100
Db	2255	GTCGCAATTAGTCAAAAGCGATGGCTCGAGCTGGAGCCCAACAACATTTGCAAAACCA	2314
Qy	2101	ATAAATACGGCAGCCCAAGCAGGAGCGCCCAACAACATTTACAGATCCCACTCTCTCCCA	2160
Db	2315	ATAAATACGGCAGCCCAAGCAGGAGCGCCCAACAACATTTACAGATCCCACTCTCTCCCA	2374
Qy	2161	GCCATCAAGATCTGCCCGAGCCCAAGAACTCTGACCCCTTAACCTTGAGGCTTACAGAA	2220
Db	2375	GCCATCAAGATCTGCCCGAGCCCAAGAACTCTGACCCCTTAACCTTGAGGCTTACAGAA	2434
Qy	2221	AGCATTTCTGACGCTCACCACTGCTGCTTGCGCTCCAGGAAATGTTCAAGTTTGACAG	2280
Db	2435	AGCATTTCTGACGCTCACCACTGCTGCTTGCGCTCCAGGAAATGTTCAAGTTTGACAG	2494
Qy	2281	TCAAAATCTCAACCAAGACCGTTCTATAGAGGAAAGCTTTGACATGGAGAGGAAACTCTG	2340
Db	2495	TCAAAATCTCAACCAAGACCGTTCTATAGAGGAAAGCTTTGACATGGAGAGGAAACTCTG	2554
Qy	2341	TTGTCTGTCTGTGCCATGTGTCCGAGAGACTTTGGGCAATCTTTGTCTGTGCAAAACCTG	2400
Db	2555	TTGTCTGTCTGTGCCATGTGTCCGAGAGACTTTGGGCAATCTTTGTCTGTGCAAAACCTG	2614
Qy	2401	ATCAGGTCCGACCGAGGAATCGAATATATACACTTTCAGGGGAGTAGTCAAGTGGCTCCAGA	2460
Db	2615	ATCAGGTCCGACCGAGGAATCGAATATATACACTTTCAGGGGAGTAGTCAAGTGGCTCCAGA	2674
Qy	2461	GGCAGCCCAAGATTTTATACCCCAATGGAGGGAATCCAAATGTTTATATCTGATGAAGAG	2520
Db	2675	GGCAGCCCAAGATTTTATACCCCAATGGAGGGAATCCAAATGTTTATATCTGATGAAGAG	2734
Qy	2521	GTTGGTCTCCGAGAGACAGACAGACACTTTGATGTGCCACCGCAGCCTGCCAGGGAA	2580
Db	2735	GTTGGTCTCCGAGAGACAGACAGACACTTTGATGTGCCACCGCAGCCTGCCAGGGAA	2794
Qy	2581	GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGCAACGATCATCTCAGACATTTGT	2640
Db	2795	GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGCAACGATCATCTCAGACATTTGT	2854
Qy	2641	AAGCAGAGAAAGATACAGATGCCCTCAGCCTTGCCCTCATGTCAAACTGAATATA	2694
Db	2855	AAGCAGAGAAAGATACAGATGCCCTCAGCCTTGCCCTCATGTCAAACTGAATATA	2908
RESULT 8			
US-10-482-834A-55			
: Sequence 55, Application US/10482834A			
: Publication NO. US2005074764A1			
: GENERAL INFORMATION:			
: APPLICANT: Mulley, John Charles			
: APPLICANT: Harlin, Louise Anne			
: APPLICANT: Dibbens, Michelle			
: APPLICANT: Wallace, Robyn			
: APPLICANT: Phillips, Hillary Amy			
: APPLICANT: Heron, Sara Elizabeth			
: APPLICANT: Berkovic, Samuel Frank			
: APPLICANT: Scheffer, Ingrid Eileen			
: APPLICANT: Bionomics Limited			
: TITLE OF INVENTION: MUTATIONS IN ION CHANNELS			
: FILE REFERENCE: 1386/17			
: CURRENT APPLICATION NUMBER: US/10/482,834A			

/ CURRENT FILING DATE: 2004-01-02
/ NUMBER OF SEQ ID NOS: 173
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 55
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-482-834A-55

Query Match 99.5%; Score 2679.6; DB 21; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2685; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAAGATGTGAGTCGCGCCGCGGACAGGTCCTGAACTCGGACCGCCAGGAGC 60
DB 215 ATGAAGATGTGAGTCGCGCCGCGGACAGGTCCTGAACTCGGACCGCCAGGAGC 274
QY 61 GACGCGCTGCTACTGCTGGGACCCGCGGCGCACGCTTGTGGCGGCGGCTGAGCCTG 120
DB 275 GACGCGCTGCTACTGCTGGGACCCGCGGCGCACGCTTGTGGCGGCGGCTGAGCCTG 334
QY 121 AGGAGAGCGCGCGGCGGACAGGAGGCGCGGATGAGCTGCTGGGAAAGCGCTCTCT 180
DB 335 AGGAGAGCGCGCGGCGGACAGGAGGCGCGGATGAGCTGCTGGGAAAGCGCTCTCT 394
QY 181 TACACGAGTACGACAGCTGCGCGCGCAACGTCAGTACCGCGGCTGCGAGACTACCTG 240
DB 395 TACACGAGTACGACAGCTGCGCGCGCAACGTCAGTACCGCGGCTGCGAGACTACCTG 454
QY 241 TACACGCTGTGAGAGACCCCGCGGCTGGGCGCTTATCTACCAAGCTTTCCTTTC 300
DB 455 TACACGCTGTGAGAGACCCCGCGGCTGGGCGCTTATCTACCAAGCTTTCCTTTC 514
QY 301 CTGTGCTTGTGCTGATTTTGTGAGTCTTCAACATCCCTGAGACAACAAATTG 360
DB 515 CTGTGCTTGTGCTGATTTTGTGAGTCTTCAACATCCCTGAGACAACAAATTG 574
QY 361 GCCTCAAGTTGCTCTTGAATCTGAGATTCTGATGATTTGCTTGTGAGTTG 420
DB 575 GCCTCAAGTTGCTCTTGAATCTGAGATTCTGATGATTTGCTTGTGAGTTG 634
QY 421 ATCATTCGAAATCGTGTGCGGCTTGTGCTGATTAAGAGATGCGAAGAGACTG 480
DB 635 ATCATTCGAAATCGTGTGCGGCTTGTGCTGATTAAGAGATGCGAAGAGACTG 694
QY 481 AGGTTGCTCGAAAGCGCTTGTGATAGATACATTTGCTTACCTTCAATAGCA 540
DB 695 AGGTTGCTCGAAAGCGCTTGTGATAGATACATTTGCTTACCTTCAATAGCA 754
QY 541 GTTGTTCGCAAAAATCAGGGTAAATATTTTTCACGCTGCACTGAGAACTCCGT 600
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QY 661 GGTTCAGTGGTTTATGCTCAGACAGAAATTAATACAGCTTGTGATAGATATTTTG 720
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DB 935 GTTCTTAATTTTTCGTCCTTCTGTCTATCTGCTGGAAGAGATGCCAATAAGAGTTT 994
QY 781 TCTACATATGAGATGCTCTGTGTGGGCACAATTGACATTAATTTGGCTATGGA 840
DB 995 TCTACATATGAGATGCTCTGTGTGGGCACAAAATTAATTAACAATTAATTTGGCTATGGA 1054
QY 841 GACAAAATCTCCCTTAATCTGGCTGGGAAATGCTTTCGACGAGCTTTCGACCTCTG 900
DB 1055 GACAAAATCTCCCTTAATCTGGCTGGGAAATGCTTTCGACGAGCTTTCGACCTCTG 1114

QY 901 ATTCTTTCTTTGCACTCTGCGCGCATTCCTTGCTGAGTTTGTCAATTAAGTACAA 960
DB 1115 ATTCTTTCTTTGCACTCTGCGCGCATTCCTTGCTGAGTTTGTCAATTAAGTACAA 1174
QY 961 GAAACAACCCGCGAGAAAACCTTTGAGAAAAGAGAAACCAAGCTGCGCACTCAATCAG 1020
DB 1175 GAAACAACCCGCGAGAAAACCTTTGAGAAAAGAGAAACCAAGCTGCGCACTCAATCAG 1234
QY 1021 TGTGTTTGGCGTATGATGAGAAATGTTTCCATTGCACTGCAACCTGGAAGCA 1080
DB 1235 TGTGTTTGGCGTATGATGAGAAATGTTTCCATTGCACTGCAACCTGGAAGCA 1294
QY 1081 CACTTGAAGGCTTGCACACCTGCAAGCCCTACCAAGAAAGAACAGGGGAGCATCAAGC 1140
DB 1295 CACTTGAAGGCTTGCACACCTGCAAGCCCTACCAAGAAAGAACAGGGGAGCATCAAGC 1354
QY 1141 AGTCAGAAAGCTTAATTTTAAGAGGAGTGGCATGCTAGCTGCGCGGCGGCGGATTT 1200
DB 1355 AGTCAGAAAGCTTAATTTTAAGAGGAGTGGCATGCTAGCTGCGCGGCGGCGGATTT 1414
QY 1201 AAGAGCCGACAAAGCTCAGTAGTGAAGAGTCCCAAGACCGACATCAAGCCGAG 1260
DB 1415 AAGAGCCGACAAAGCTCAGTAGTGAAGAGTCCCAAGACCGACATCAAGCCGAG 1474
QY 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACGAAACCGCTTCCGCGCC 1320
DB 1475 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACGAAACCGCTTCCGCGCC 1534
QY 1321 TCGCTGCGCTTCAAAAATTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCTTGGC 1380
DB 1535 TCGCTGCGCTTCAAAAATTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCTTGGC 1594
QY 1381 ACTGATGATGATATGATGAGAAAAGAGTCCAGTGTGATGATCAGTGAAGAGCTCAAC 1440
DB 1595 ACTGATGATGATATGATGAGAAAAGAGTCCAGTGTGATGATCAGTGAAGAGCTCAAC 1654
QY 1441 CCACCACTTAAACCTGATTCAGCTATCAGATTAAGAAATTTTCAATGTTGCAAAACGG 1500
DB 1655 CCACCACTTAAACCTGATTCAGCTATCAGATTAAGAAATTTTCAATGTTGCAAAACGG 1714
QY 1501 AAGTTAAGGAAACCTTACGTCATATGATTAAGTATGATTAAGTATGATTAATTCGCT 1560
DB 1715 AAGTTAAGGAAACCTTACGTCATATGATTAAGTATGATTAAGTATGATTAATTCGCT 1774
QY 1561 GGTCACTGCAATGTTGTGATTAAGTATTAAGCTTCAACACGCTGATCAAAATTCCT 1620
DB 1775 GGTCACTGCAATGTTGTGATTAAGTATTAAGCTTCAACACGCTGATCAAAATTCCT 1834
QY 1621 GGAAGAGGCAAAATCAGATCAGATTAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1680
DB 1835 GGAAGAGGCAAAATCAGATCAGATTAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1894
QY 1681 ACCACAGACATTCAGATATGCTGCGTGGGTGCTGCAAGTTTGAAGAACAGTTAAGTCC 1740
DB 1895 ACCACAGACATTCAGATATGCTGCGTGGGTGCTGCAAGTTTGAAGAACAGTTAAGTCC 1954
QY 1741 ATAGAGTCCAAGCTGCACTGCTACTAGACATTAACAAGTCTCTCGAAAAGCTCT 1800
DB 1955 ATAGAGTCCAAGCTGCACTGCTACTAGACATTAACAAGTCTCTCGAAAAGCTCT 2014
QY 1801 GCTCAGCCCTGCTTGGCTTCAATTCAGATTCACACTTTTGAATGTAACAGACATCT 1860
DB 2015 GCTCAGCCCTGCTTGGCTTCAATTCAGATTCACACTTTTGAATGTAACAGACATCT 2074
QY 1861 GACTATCAAAAGCCCTGAGATGAGAAAGATCTTTCGAGTTCCGACAAAGAGTGGTGC 1920
DB 2075 GACTATCAAAAGCCCTGAGATGAGAAAGATCTTTCGAGTTCCGACAAAGAGTGGTGC 2134
QY 1921 TTATCAGATCAACTAGTGCACATCTCGAGAGGCTGCAAGTTCAATCTGACGCAAT 1980
DB 2135 TTATCAGATCAACTAGTGCACATCTCGAGAGGCTGCAAGTTCAATCTGACGCAAT 2194
QY 1981 GAGTTCAAGTCCAGACATTTCTAGCGGCTTACCTTACTATGACAGTCAAGCAACAG 2040

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Db 2195 GAGTTGAGTGGCCAGACTTTCTAGGCGCTTAGCCCTTAGTGAACAGTACAGCAACAG 2254
Qy 2041 GTGCCAATTAGTCAAAAGCGATGGCTGACGAGTGGACCCCAACACCATTTGAAACCAA 2100
Db 2255 GTGCCAATTAGTCAAAAGCGATGGCTGACGAGTGGACCCCAACACCATTTGAAACCAA 2314
Qy 2101 ATAAATACGGCAGCCCAAGCCAGAGCCCAACAACTTTATAGATGCCACCTCCCTCCCA 2160
Db 2315 ATAAATACGGCAGCCCAAGCCAGAGCCCAACAACTTTATAGATGCCACCTCCCTCCCA 2374
Qy 2161 GCCATACAGCATCTGCCAGAGCCCAAACTCTGCACTTAACTCCAGGCTTTACAGAA 2220
Db 2375 GCCATACAGCATCTGCCAGAGCCCAAACTCTGCACTTAACTCCAGGCTTTACAGAA 2434
Qy 2221 AGCATTTCTGACGTCAACCACTGCTTTGCTTGGCTCCAGAGAAATGTTCAAGTTGACAG 2280
Db 2435 AGCATTTCTGACGTCAACCACTGCTTTGCTTGGCTCCAGAGAAATGTTCAAGTTGACAG 2494
Qy 2281 TCMAATCTCAACAAGACCGTTCTATGAGGAAAGCTTTGACATGGAGAGAAACTCTG 2340
Db 2495 TCMAATCTCAACAAGACCGTTCTATGAGGAAAGCTTTGACATGGAGAGAAACTCTG 2554
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Db 2615 ATCAGGTCCAGCCAGAGACGTAATATACAACTTTACAGGAGTGAATGCTGCTCCAGA 2674
Qy 2461 GGCAGCCAGATTTTATCCCAATAGAGGAAATCCAAATTTGTTTAACTGATGAAGAG 2520
Db 2675 GGCAGCCAGATTTTATCCCAATAGAGGAAATCCAAATTTGTTTAACTGATGAAGAG 2734
Qy 2521 GTGGGTCCTCCAGAGACAGAGACAGACATTTTGTATGTCGCGACCGAGCTGCGAGGAA 2580
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Qy 2581 GCTGCTTTGTCATCAACTCTCTAAGAGCTGGAAGTCAAGATCACTCAGAGCAATTTGT 2640
Db 2795 GCTGCTTTGTCATCAACTCTCTAAGAGCTGGAAGTCAAGATCACTCAGAGCAATTTGT 2854
Qy 2641 AAGGCAAGAGAAATGACAGATGCCCTCAGCTTGCCTCATGTCAACTGAATAA 2694
Db 2855 AAGGCAAGAGAAATGACAGATGCCCTCAGCTTGCCTCATGTCAACTGAATAA 2908

RESULT 9
US-09-810-796-3
; Sequence 3: Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeggla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCMQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCMQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCMQ5-2
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US-09-810-796-3
Query Match 97.6%; Score 2630; DB 9; Length 2667;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

Qy 1 ATGAAGATGTGAGTGGGCGGCGGAGGAGGAGTGTCTGTAACCTCGACAGCCGACAGGCG 60
Db 1 ATGAAGATGTGAGTGGGCGGCGGAGGAGGAGTGTCTGTAACCTCGACAGCCGACAGGCG 60
Qy 61 GAGGCGCTCTACTGCTGGGACACCCGCGCGCACGCTTGTGGCGCGCGGCTGCTG 120
Db 61 GAGGCGCTCTACTGCTGGGACACCCGCGCGCACGCTTGTGGCGCGCGGCTGCTG 120
Qy 121 AGGAGAGCGCGCGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 121 AGGAGAGCGCGCGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 181 TACACGATGAGCAGAGTGGCGGCGCAAGTCAAGTACCGGCGGAGTGCAGAACTACTG 240
Db 181 TACACGATGAGCAGAGTGGCGGCGCAAGTCAAGTACCGGCGGAGTGCAGAACTACTG 240
Qy 241 TACACGATGAGCAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 TACACGATGAGCAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 301 CTGTGCTTTGCTGCTGATTTTGTGAGTGTCTTCAACATCCCTGAGACACAAATTTG 360
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Qy 361 GCTCAAGTTGCTCTTGAATCCCTGAGTTCGATGATTTGTGCTTGTGTTGAGTTG 420
Db 361 GCTCAAGTTGCTCTTGAATCCCTGAGTTCGATGATTTGTGCTTGTGTTGAGTTG 420
Qy 421 ATCATTTGATGATGTCGTCGCGGCTGCTGTGTGATATAGATGAGATGCAAGAGACTG 480
Db 421 ATCATTTGATGATGTCGTCGCGGCTGCTGTGTGATATAGATGAGATGCAAGAGACTG 480
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Db 601 TTCTTACAGATCTCTCGCATGGTGGCATGACCGAAGGAGAGCACTTGAATTTACTG 660
Qy 661 GGTTCAGTGTGTATGCTCAGACAGAAATTAATACAGCTTGTGATACATTTTGTG 720
Db 661 GGTTCAGTGTGTATGCTCAGACAGAAATTAATACAGCTTGTGATACATTTTGTG 720
Qy 721 GTTCTTATTTTGTGCTTCTTCTGTCTATCTGTGAGAAAGATTAAGAGTTT 780
Db 721 GTTCTTATTTTGTGCTTCTTCTGTCTATCTGTGAGAAAGATTAAGAGTTT 780
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Db 781 TCTACATATGAGATGCTCTGTGTGGGCAATTAATTAACAATTAATTTGCTATGGA 840
Qy 841 GACAAACCTCCCTAATCTGTGGGAGATTTGCTTGCAGGCTTGTGACCTCTTGGC 900
Db 841 GACAAACCTCCCTAATCTGTGGGAGATTTGCTTGCAGGCTTGTGACCTCTTGGC 900
Qy 901 ATTTCTTTTGTGACTTCTGCTCCGCAATCTTGTGCTCAGTTTGTGATTAAGTACA 960
Db 901 ATTTCTTTTGTGACTTCTGCTCCGCAATCTTGTGCTCAGTTTGTGATTAAGTACA 960
Qy 961 GAACAAACCGCCAGAAACATTTGAGAAAGAGAAACCAAGTGCACCACTCATTCAG 1020
Db 961 GAACAAACCGCCAGAAACATTTGAGAAAGAGAAACCAAGTGCACCACTCATTCAG 1020
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QY 1021 TGTGTTGGCGTAGTGAAGCAAGTGAAGAACTGTTTCCATTGCAACTGGAAAGCCA 1080
DB 1021 TGTGTTGGCGTAGTGAAGCAAGTGAAGAACTGTTTCCATTGCAACTGGAAAGCCA 1080
QY 1081 CACTGGAAGGCTTGGACACTGGACGCTTACCAAGAAAAGAACAGGGAAGCATCAAGC 1140
DB 1081 CACTGGAAGGCTTGGACACTGGACGCTTACCAAGAAAAGAACAGGGAAGCATCAAGC 1140
QY 1141 AGTCAGAACTAAGTTTAAAGGACGAGTGGCATGGCTAGCCCCAGGGGACGAGTATT 1200
DB 1116 ---TCAGAACTAAGTTTAAAGGACGAGTGGCATGGCTAGCCCCAGGGGACGAGTATT 1173
QY 1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGACCCGACATCAAGCCGAG 1260
DB 1174 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGACCCGACATCAAGCCGAG 1233
QY 1261 GGCAGTCCCAAGAAAGTGAAGAAAGCTGAGCTTCAAGACCCGCTTCCGGCCC 1320
DB 1234 GGCAGTCCCAAGAAAGTGAAGAAAGCTGAGCTTCAAGACCCGCTTCCGGCCC 1293
QY 1321 TCGCTGCGCTCAAAAAGTTCTGACCCAAACAGTATGATGTCGACAGCCCTTGGC 1380
DB 1294 TCGCTGCGCTCAAAAAGTTCTGACCCAAACAGTATGATGTCGACAGCCCTTGGC 1353
QY 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
QY 1441 CCACCACTTAAACCTGCTAGTGGAGTATCAGAAATTATGAAATTTTCAATGTTCAAAACG 1500
DB 1414 CCACCACTTAAACCTGCTAGTGGAGTATCAGAAATTATGAAATTTTCAATGTTCAAAACG 1473
QY 1501 AAGTTTAAAGAAACGTTACGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
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QY 1561 GGTGATCTGGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1534 GGTGATCTGGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
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DB 1594 GGAAGAAAGGCAATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
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QY 1741 ATAGAGTCCAAAGCTGATGCTGCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1714 ATAGAGTCCAAAGCTGATGCTGCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
QY 1801 GCTCAGAGCTGCTGCTTGGCTCATTTCCAGATCCCACTTTGAAATGTAAGACAGATCT 1860
DB 1774 GCTCAGAGCTGCTGCTTGGCTCATTTCCAGATCCCACTTTGAAATGTAAGACAGATCT 1833
QY 1861 GACTATCAAAAGCCCTGTGATGACAAAGATCTTTGGGTTCCGCAAAAGAGTGGCTGC 1920
DB 1834 GACTATCAAAAGCCCTGTGATGACAAAGATCTTTGGGTTCCGCAAAAGAGTGGCTGC 1893
QY 1921 TTATCCAGATCAACTAGTCCCAACATCTTGAGAGGCTTGCAAGTCAATTTGACGCCAAT 1980
DB 1894 TTATCCAGATCAACTAGTCCCAACATCTTGAGAGGCTTGCAAGTCAATTTGACGCCAAT 1953
QY 1981 GAGTTCAAGGCCCAAGCTTTCAAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2040
DB 1954 GAGTTCAAGGCCCAAGCTTTCAAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2013
QY 2041 GTGCCAATTATGTCAAAGCGATGGCTCAGCAGTGGACGCCCAACAGCACTTGGCAACCA 2100
DB 2014 GTGCCAATTATGTCAAAGCGATGGCTCAGCAGTGGACGCCCAACAGCACTTGGCAACCA 2073
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QY 2101 ATAAATACGGGACCCCAAGCCAGACGCCCCCAACCACTTTACAGATCCACTCTCTCCCA 2160
DB 2074 ATAAATACGGGACCCCAAGCCAGACGCCCCCAACCACTTTACAGATCCACTCTCTCCCA 2133
QY 2161 GGCATCAAGCATCTGCCCCAGGCGAAGAACTCTGCAACCCCTTAACCCGAGGCTTAAGGAA 2220
DB 2134 GGCATCAAGCATCTGCCCCAGGCGAAGAACTCTGCAACCCCTTAACCCGAGGCTTAAGGAA 2193
QY 2221 AGCATTTTGAAGTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
DB 2194 AGCATTTTGAAGTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2253
QY 2281 TCAAAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGAGAGAGAACTCTG 2340
DB 2254 TCAAAATTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGAGAGAGAACTCTG 2313
QY 2341 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
DB 2314 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2373
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DB 2374 ATCAGGTGACCGAGGAACTGAATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2433
QY 2461 GGCAGCCAAATTTTACCCCAATGAGGGAATCCAAATTTTATTAATCTGATGAAG 2520
DB 2434 GGCAGCCAAATTTTACCCCAATGAGGGAATCCAAATTTTATTAATCTGATGAAG 2493
QY 2521 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCGACCGGACCTGCCAGGGA 2580
DB 2494 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCGACCGGACCTGCCAGGGA 2553
QY 2581 GCTGCTTTGATCAGACTCTCTAAGACTGGAAGTCAAGATCTCAGAGCAATTTGT 2640
DB 2554 GCTGCTTTGATCAGACTCTCTAAGACTGGAAGTCAAGATCTCAGAGCAATTTGT 2613
QY 2641 AAGCAGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2694
DB 2614 AAGCAGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2667

RESULT 10
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US2002042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehl, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US2002042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FID REFERENCE: LEX-0160-USA
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 97.4%; Score 2625.2; DB 9; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTGGGCGGCGGAGGAGTGTGCTGTAACCTGGAGCCGCCAGGGGC 60
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106 ATGAGATGTGAGTGGGCGGAGGAGGTGCTGTAACCTCGGACGCGCAAGGGG 165
QY 61 GAGGGCTGTACTGCTGGGACCCGCGGCCACGCTGTGTGGCGGCGGTGGCTTG 120
Db 166 GAGGGCTGTACTGCTGGGACCCGCGGCCACGCTGTGTGGCGGCGGTGGCTTG 225
QY 121 AGGAGAGCGCGGAGGAGCAAGAGGGGGCCCGGATGAGCTGTGTGGGGAAGCCCTCTT 180
Db 226 AGGAGAGCGCGGAGGAGCAAGAGGGGGCCCGGATGAGCTGTGTGGGGAAGCCCTCTT 285
QY 181 TACACGAGTAGCAGAGCTGCCGCGCAACGTCAGACCGGCGGTGCAGAACTACCTG 240
Db 286 TACACGAGTAGCAGAGCTGCCGCGCAACGTCAGACCGGCGGTGCAGAACTACCTG 345
QY 241 TACACGAGTAGCAGAGCAACCCCGCGGTGGCGTTCATCTACACGCTTCTGTTTTCTC 300
Db 346 TACACGAGTAGCAGAGCAACCCCGCGGTGGCGTTCATCTACACGCTTCTGTTTTCTC 405
QY 301 CTGTGCTTGTGCTTGAATTTTGTCAAGTGTTCATCCCTGAGCACACAAATTG 360
Db 406 CTGTGCTTGTGCTTGAATTTTGTCAAGTGTTCATCCCTGAGCACACAAATTG 465
QY 361 GCGTCAAGTTGCGCTTGTGATCTGAGATTGCTGATGATGTCGTCCTTGGTTTGAAGTTC 420
Db 466 GCGTCAAGTTGCGCTTGTGATCTGAGATTGCTGATGATGTCGTCCTTGGTTTGAAGTTC 525
QY 421 ATCATTCGAAATCTGCTGTGGGGTGTCTGTTCGATATAGAGATGAGCAGAGAACTG 480
Db 526 ATCATTCGAAATCTGCTGTGGGGTGTCTGTTCGATATAGAGATGAGCAGAGAACTG 585
QY 481 AGGTTTGCTGGAAGCCCTCTGTGTATATAGATACCATGTTCTTATGCTTCATATAGCA 540
Db 586 AGGTTTGCTGGAAGCCCTCTGTGTATATAGATACCATGTTCTTATGCTTCATATAGCA 645
QY 541 GTTGTTCCTGCAAAACTCAGGGTAAATATTTTTCGACGCTGCACTCAGAACTCCGT 600
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QY 601 TTCCTACAGATCTCCGCGATGTGGCCATGAGACCGAAAGGGGAGCACTTGGAAATTACTG 660
Db 706 TTCCTACAGATCTCCGCGATGTGGCCATGAGACCGAAAGGGGAGCACTTGGAAATTACTG 765
QY 661 GGTTGAGTGATGCTCTCAGCAGAGAAATTAATCAGAGCTGTGATACATAGGATTTTGG 720
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QY 781 TCTACATATGCAATGCTCTCTGTGTGGGCAAAATTAATGACATATATGCTATGGA 840
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Db 1006 ATTTCTTTCTTTGACATTCCTGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACA 1065
QY 961 GAACCAACCCGCGAGAAACATTTGAGAAAAAGAAAGAACCCAGCTGCCAATCTTACG 1020
Db 1066 GAACCAACCCGCGAGAAACATTTGAGAAAAAGAAAGAACCCAGCTGCCAATCTTACG 1125
QY 1021 TGTGTTGGGAGTATGAGCAGCTGATGAGAAATCTGTTCCATTCGAACCTGGAAGCA 1080
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QY 1081 CACTTGAAGGCTTGCACACTGACGCTTACCAAGAAAGAACAGGGAGCATCAAGC 1140
1186 CACTTGAAGGCTTGCACACTGACGCTTACCA----- 1220
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Db 1221 --TCAGAACTAAGTTTAAAGAGCGAGTCCGATGCTAGCCCGAGGGGCGAGATATT 1278
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Db 1279 AAGAGCGCAAGAGCTCAGTAAGTGAACAGAGGTCCCAAGCACGACATCAAGCGAG 1338
QY 1261 GGCAGTCCCAAGAGTCAGAAAGAGCTGAGCTTCAACGACCGAAACCCGCTTCGCGCC 1320
Db 1339 GGCAGTCCCAAGAGTCAGAAAGAGCTGAGCTTCAACGACCGAAACCCGCTTCGCGCC 1398
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Db 1399 TCGCTGGGCTCAAAAGTTCTCAGCCCAACAGATATGATGCTGACACAGCCCTTGGC 1458
QY 1381 ACTGATGATATATGATGAAAAAGGATGCAAGTGTATGATGAGAGACCTCAC 1440
Db 1459 ACTGATGATATATGATGAAAAAGGATGCAAGTGTATGATGAGAGACCTCAC 1518
QY 1441 CCAACAATTAAACCTGTATTCGAGCTATCAGAAATTGAAATTCATGTTGCAAAACG 1500
Db 1519 CCAACAATTAAACCTGTATTCGAGCTATCAGAAATTGAAATTCATGTTGCAAAACG 1578
QY 1501 AAGTTTAAAGAAACGTTAGTCCATATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1579 AAGTTTAAAGAAACGTTAGTCCATATGATGATGATGATGATGATGATGATGATGAT 1638
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Db 1879 GCGTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTGAAATGTAACAGACATCT 1938
QY 1861 GACTATCAAGAGCCGTGTGATGCAAAAGATCTTTGGGGTTCGCGCAAAACAGTGGCTGC 1920
Db 1939 GACTATCAAGAGCCGTGTGATGCAAAAGATCTTTGGGGTTCGCGCAAAACAGTGGCTGC 1998
QY 1921 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCAATTCATTCGAGCGCAAT 1980
Db 1999 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCAATTCATTCGAGCGCAAT 2058
QY 1981 GAGTTCAGTGCAGACTTTCAGCGGCTTACGCTTACTATGCAAGTCAACACACAG 2040
Db 2059 GAGTTCAGTGCAGACTTTCAGCGGCTTACGCTTACTATGCAAGTCAACACACAG 2118
QY 2041 GTGCCAATTATGTCAAAGAGATGGCTCAGAGTGGAGCCACCAACATTTGCAAAACCA 2100
Db 2119 GTGCCAATTATGTCAAAGAGATGGCTCAGAGTGGAGCCACCAACATTTGCAAAACCA 2178
QY 2101 ATAAATACGCGCAACCAAGCAGACAGCCCAACCACTTTACAGATCCACCTTCTCCCA 2160
Db 2179 ATAAATACGCGCAACCAAGCAGACAGCCCAACCACTTTACAGATCCACCTTCTCCCA 2238
QY 2161 GCCATCAGACATCTGCGCCAGGCGCAAGAACTCTGACACCTTACAGGCTTACAGGAA 2220
Db 2239 GCCATCAGACATCTGCGCCAGGCGCAAGAACTCTGACACCTTACAGGCTTACAGGAA 2298
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Qy	2221	AGCATTTCTGACGCGTACCACTGCTGTGGCTCCAAAGAAATGTCAGCTGCACAG	2280
Db	2299	AGCATTTCTGACGTCACCACTGCTGTGGCTCCAAAGAAATGTCAGCTGCACAG	2358
Qy	2281	TCAAAATCTCAACCAAGACCGTTCTTATGAGAAAAAGCTTTGACATGGAGGAAACTCTG	2340
Db	2359	TCAAAATCTCAACCAAGACCGTTCTTATGAGAAAAAGCTTTGACATGGAGGAAACTCTG	2418
Qy	2341	TTGTCTGTCTGTCCCATGTGTCCGAAAGACCTTGGGCAATCTTTGTCTGTGCCAAACTGT	2400
Db	2419	TTGTCTGTCTGTCCCATGTGTCCGAAAGACCTTGGGCAATCTTTGTCTGTGCCAAACTGT	2478
Qy	2401	ATCAGGTGCAACCGAGAACTGAATATACAACTTTTCAGGGAGTGAATCAAGTGGCTCCAGA	2460
Db	2479	ATCAGGTGCAACCGAGAACTGAATATATACAACTTTTCAGGGAGTGAATCAAGTGGCTCCAGA	2538
Qy	2461	GGCAGCCAGATTTTATACCCCAATGTGAGGGAAATCCAAATGTTTATATCTGATGAAGAG	2520
Db	2539	GGCAGCCAGATTTTATACCCCAATGTGAGGGAAATCCAAATGTTTATATCTGATGAAGAG	2598
Qy	2521	GTGGGTCCCGAAGACAGACAGACACTTTTATGTCCGACCGGACCTGCCAGGGAA	2580
Db	2599	GTGGGTCCCGAAGACAGACAGACACTTTTATGTCCGACCGGACCTGCCAGGGAA	2658
Qy	2581	GCTTCCTTTGGCATCAGACTCTCTAAGAGCTGGAAGTTCACGATCATCTCAGAGCAATTTGT	2640
Db	2659	GCTTCCTTTGGCATCAGACTCTCTAAGAGCTGGAAGTTCACGATCATCTCAGAGCAATTTGT	2718
Qy	2641	AAGCAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCCAAACTGAATTA	2694
Db	2719	AAGCAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCCAAACTGAATTA	2772

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RESULT 11
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

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Query Match	97.4%	Score 2625.2;	DB 19;	Length 2772;
Best Local Similarly	98.9%	Pred. No. 0;		
Matches 2664; Conservative	0;	Mismatches	3;	Indels 27; Gaps 1;

QY 1 ATGAAGATGTGGAGTCCGGCCGGGGGACAGGGTGTCTGTGAACCTGGACACGGCCAGAGGGC 60
Db 106 ATGAAGATGTGGAGTCCGGCCGGGGGACAGGGTGTCTGTGAACCTGGACACGGCCAGAGGGGC 165
QY 61 GACGGCTGTACTGTCTGGGGCACCCGGCGGCCAAGCTTGGTGGGGGGGGGGTGGCCTTG 120

Db	166	GACGGCTGCTACTGCTGGGACACCCGGGCGGACACGTCGGTGGCGGCGGCGTGGGCTG	225
OY	121	AGGGAAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCGGGAAAGCGCTCTCT	180
Db	226	AGGGAAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCGGGAAAGCGCTCTCT	285
OY	181	TACACGAGTAGCCGAGAGCTGCGGGCGAACGTCAGTAACCGGGCGGGTGACGAATCTACTG	240
Db	286	TACACGAGTAGCCGAGAGCTGCGGGCGAACGTCAGTAACCGGGCGGGTGACGAATCTACTG	345
OY	241	TACACGAGTAGAGAGACCCCGGGCGTGGCGGTTCATCTACACGCTTTGTTTTCTC	300
Db	346	TACACGAGTAGAGACCCCGGGCGTGGCGGTTCATCTACACGCTTTGTTTTCTC	405
OY	301	CTTGCTTTGGTGCTGATTTTGTCAAGTTTTCTACATCCCTGAGCACACAAATTG	360
Db	406	CTTGCTTTGGTGCTGATTTTGTCAAGTTTTCTACATCCCTGAGCACACAAATTG	465
OY	361	GCCCTAAGTGGCCTTGATCTCGAGATCGTAGTAGTTGTCGTCCTTGGTTGGAGTTC	420
Db	466	GCCCTAAGTGGCCTTGATCTCGAGATCGTAGTAGTTGTCGTCCTTGGTTGGAGTTC	525
OY	421	ATCATTTGAATCTGGTCTGGGGGTTCGTGTTTCGATATAGAGATGGCAAGAAAGCTG	480
Db	526	ATCATTTGAATCTGGTCTGGGGGTTCGTGTTTCGATATAGAGATGGCAAGAAAGCTG	585
OY	481	AGGTTTCTCGAAAGCCCTTCTGTGTATATAGATACCATTTGTCCTTACGCTTCAATAGCA	540
Db	586	AGGTTTCTCGAAAGCCCTTCTGTGTATATAGATACCATTTGTCCTTACGCTTCAATAGCA	645
OY	541	GTTGTTTCTGCAAAAACCTCAGGGTATATATTTTTCGACGTCCTGCACTCAGAAAGTCTCCGT	600
Db	646	GTTGTTTCTGCAAAAACCTCAGGGTATATATTTTTCGACGTCCTGCACTCAGAAAGTCTCCGT	705
OY	601	TTCTTACAGATCCCTCGCATGGTGGCGATGAGCCGAAGGGGAGGCACTTGGAAATTACTG	660
Db	706	TTCTTACAGATCCCTCGCATGGTGGCGATGAGCCGAAGGGGAGGCACTTGGAAATTACTG	765
OY	661	GGTTCAGTGGTTATAGCTCACAGCAAGAAATTATACACAGCTTGTGATCATAGATTTTTG	720
Db	766	GGTTCAGTGGTTATAGCTCACAGCAAGAAATTATACACAGCTTGTGATCATAGATTTTTG	825
OY	721	GTTCTTATATTTTGGTCTTCTTCCCTTGTCTATCTGTGAAAAAGATGGCAATTAAGACTTT	780
Db	826	GTTCTTATATTTTGGTCTTCTTCCCTTGTCTATCTGTGAAAAAGATGGCAATTAAGACTTT	885
OY	781	TCTACATATGAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTTGGCTATAGA	840
Db	886	TCTACATATGAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTTGGCTATAGA	945
OY	841	GACAAAACCTCCCTAACCTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTTGGC	900
Db	946	GACAAAACCTCCCTAACCTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTTGGC	1005
OY	901	ATTTCCTTCTTTGGACCTTCCGCGGGGATTTCTTGGCTCAGAGTTTTTGCAATTAAGTACAA	960
Db	1006	ATTTCCTTCTTTGGACCTTCCGCGGGGATTTCTTGGCTCAGAGTTTTTGCAATTAAGTACAA	1065
OY	961	GAACAAACCGCCGAGAAACCTTTGAAAAAAGAAAGCCGAGCTGCAACTTCATTCAAG	1020
Db	1066	GAACAAACCGCCGAGAAACCTTTGAAAAAAGAAAGCCGAGCTGCAACTTCATTCAAG	1125
OY	1021	TGTCCTTTGGGTAGTTAGCAGCTGAGAGAAATCTGTTCCATTTGCAACCTGGAAAGCA	1080
Db	1126	TGTCCTTTGGGTAGTTAGCAGCTGAGAGAAATCTGTTCCATTTGCAACCTGGAAAGCA	1185
OY	1081	CACTTGAAAGGCTTGCACACCTGACGCGCTTACCAAGAAAGAAAGCAAGGGGAAGCATCAAGC	1140
Db	1186	CACTTGAAAGGCTTGCACACCTGACGCGCTTACCAAGAAAGAAAGCAAGGGGAAGCATCAAGC	1220
OY	1141	AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATAGCTTACCGGCGCCAGAGTATTT	1200
Db	1221	--TCAGAGCTAAGTTTAAAGAGCGAGTGGCATAGCTTACCGGCGCCAGAGTATTT	1278

|||||
Db 345 TACACAGTAGCAGAGCTGCGCGCAAGTCAATGACCGGGGGTGCAGAACTACTCTG 404
QY 241 TACAAAGTGTGAGAGAGACCCCGGGCTGGGCTTATCTACACAGCTTTCGTTTTCTC 300
Db 405 TACAAAGTGTGAGAGAGACCCCGGGCTGGGCTTATCTACACAGCTTTCGTTTTCTC 464
QY 301 CTGTCTTGGTGTGATGATTTTGTGAGTTCCTTACCATCCCTGAGACACAAATTG 360
Db 465 CTGTCTTGGTGTGATGATTTTGTGAGTTCCTTACCATCCCTGAGACACAAATTG 524
QY 361 GCGTCAAGTTGCGCTTTGATCCTGAGTTGAGTATGTCGTTCTTTGGATTTC 420
Db 525 GCGTCAAGTTGCGCTTTGATCCTGAGTTGAGTATGTCGTTCTTTGGATTTC 584
QY 421 ATCATTCGAATCTGCTGCGGGTTCGTTGCTATGAGATGAGAGAGCAAGAACTG 480
Db 585 ATCATTCGAATCTGCTGCGGGTTCGTTGCTATGAGATGAGAGAGCAAGAACTG 644
QY 481 AGGTTGCTGAAAAGCCCTTCTGTGTATAGATACCATTTCTTATCGCTCAATAGCA 540
Db 645 AGGTTGCTGAAAAGCCCTTCTGTGTATAGATACCATTTCTTATCGCTCAATAGCA 704
QY 541 GTTGTTCGCAAAAACCTCAGGGTAATATTTTGCACGCTGCACTCAGAACTCCGT 600
Db 705 GTTGTTCGCAAAAACCTCAGGGTAATATTTTGCACGCTGCACTCAGAACTCCGT 764
QY 601 TTCCTACATCTCTCGGCAATGTCGCGCATGAGACCGAAGGGAGGCACTTGAATTAATG 660
Db 765 TTCCTACATCTCTCGGCAATGTCGCGCATGAGACCGAAGGGAGGCACTTGAATTAATG 824
QY 661 GGTTCAAGTGTATGCTCACAAGCAAGATTAATCAGAGTTGATAGATTAAGATTG 720
Db 825 GGTTCAAGTGTATGCTCACAAGCAAGATTAATCAGAGTTGATAGATTAAGATTG 884
QY 721 GTTCTTATTTTTCGTTCTTCTTCTGTAATCTGTGAAAAGAGATCAATAAAGATT 780
Db 885 GTTCTTATTTTTCGTTCTTCTTCTGTAATCTGTGAAAAGAGATCAATAAAGATT 944
QY 781 TCTACATATGAGATGCTCTGTGAGGGGCAAAATTAATGAACTATGAGCTATGAG 840
Db 945 TCTACATATGAGATGCTCTGTGAGGGGCAAAATTAATGAACTATGAGCTATGAG 1004
QY 841 GACAAAACCTCCCTTAATGCTGAGGAGATGCTTCTGCAAGGCTTTCACCTCTGGC 900
Db 1005 GACAAAACCTCCCTTAATGCTGAGGAGATGCTTCTGCAAGGCTTTCACCTCTGGC 1064
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCAATTTTGGCTCAGGTTTTCATTAAAGTACA 960
Db 1065 ATTTCTTTCTTTGCACTTCTGCGGCAATTTTGGCTCAGGTTTTCATTAAAGTACA 1124
QY 961 GAAACAACACGCGCAGAAACATTTGAAAAGAGAACCCAGCTGCCAACCCTCAATG 1020
Db 1125 GAAACAACACGCGCAGAAACATTTGAAAAGAGAACCCAGCTGCCAACCCTCAATG 1184
QY 1021 TGTGTTTGGCTGATGATGCTGAGCTGATGAAATCTGTTCCATTGCAACTGGAAGCA 1080
Db 1185 TGTGTTTGGCTGATGATGCTGAGCTGATGAAATCTGTTCCATTGCAACTGGAAGCA 1244
QY 1081 CACTTGAAAGGCTTGCACACTGCAAGCCCTTACCAAGAAAGAAACAAGGGAGATCAAGC 1140
Db 1245 CACTTGAAAGGCTTGCACACTGCAAGCCCTTACCA----- 1279
QY 1141 AGTCGAAGCTAAGTTTAAAGAGAGATGCGCATGGCTAGCCCAAGGGGCGAGATAT 1200
Db 1280 --TCGAAGCTAAGTTTAAAGAGAGATGCGCATGGCTAGCCCAAGGGGCGAGATAT 1337
QY 1201 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGGTCCCAAGCACGCAATCAAGCCGAG 1260
Db 1338 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGGTCCCAAGCACGCAATCAAGCCGAG 1397
QY 1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCCGGCCC 1320
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Db 1398 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCCGGCCC 1457
QY 1321 TCGTGGCCCTCAAAAGTTCTCAGCCAAACCAAGATATGATGCTGACACAGCCCTTGGC 1380
Db 1458 TCGTGGCCCTCAAAAGTTCTCAGCCAAACCAAGATATGATGCTGACACAGCCCTTGGC 1517
QY 1381 ACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCAGTGAAGACCTCAC 1440
Db 1518 ACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCAGTGAAGACCTCAC 1577
QY 1441 CCACCATTAAAACTGTCATTCGAGCTATCGAATTAATGAATTTTATGTTGCAAAACGG 1500
Db 1578 CCACCATTAAAACTGTCATTCGAGCTATCGAATTAATGAATTTTATGTTGCAAAACGG 1637
QY 1501 AAGTTAAGAAAGTTACGTCCATGATGATGAAAAAGTGCATTTGACATTAATTCGCT 1560
Db 1638 AAGTTAAGAAACCTTACGTCCATGATGATGAAAAAGTGCATTTGACATTAATTCGCT 1697
QY 1561 GGTCACTGACATGTTGTGTAATTTAAAGCCTTCAAAACGCTGTGATCAAAATTCCT 1620
Db 1698 GGTCACTGACATGTTGTGTAATTTAAAGCCTTCAAAACGCTGTGATCAAAATTCCT 1757
QY 1621 GAAAAAGGGCAATCAATCAGATTAAGAAAGCCGAGAGAAATTAACGACGAACATGAG 1680
Db 1758 GAAAAAGGGCAAAATCAATCAGATTAAGAAAGCCGAGAGAAATTAACGACGAACATGAG 1817
QY 1681 ACCACAGACGATCTCAGTATGCTGCTGGGTGGTCAAGTTGAAAAACAGTACAGTCC 1740
Db 1818 ACCACAGACGATCTCAGTATGCTGCTGGGTGGTCAAGTTGAAAAACAGTACAGTCC 1877
QY 1741 ATAGAGTCAAGCTGACCTGCTACTAGACATCTATCAACAGTCTTTCGAAAAAGCTCT 1800
Db 1878 ATAGAGTCAAGCTGACCTGCTACTAGACATCTATCAACAGTCTTTCGAAAAAGCTCT 1937
QY 1801 GCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTAACAGATCT 1860
Db 1938 GCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTAACAGATCT 1997
QY 1861 GACTATCAAAAGCCCTGAGATAGCAAAAGATCTTTCGGGTTCGCAAAACAGTGGCTGC 1920
Db 1998 GACTATCAAAAGCCCTGAGATAGCAAAAGATCTTTCGGGTTCGCAAAACAGTGGCTGC 2057
QY 1921 TTATCCAGATCAATGATGCCAATCTCGAAGAGCCCTGCAATTCATTCGACGCCAAT 1980
Db 2058 TTATCCAGATCAATGATGCCAATCTCGAAGAGCCCTGCAATTCATTCGACGCCAAT 2117
QY 1981 GAGTTCAAGTCCAGACTTTCTAGCGCTTAGCCCTATATGACAGTCAACCAACAG 2040
Db 2118 GAGTTCAAGTCCAGACTTTCTAGCGCTTAGCCCTATATGACAGTCAACCAACAG 2177
QY 2041 GTGCCAATTTAGTCAAAAGGATGGCTCAGCAGTGGGAGCACAACACCATTTGCAACCA 2100
Db 2178 GTGCCAATTTAGTCAAAAGGATGGCTCAGCAGTGGGAGCACAACACCATTTGCAACCA 2237
QY 2101 ATTAATACGAGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCACTCTCTCCA 2160
Db 2238 ATTAATACGAGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCACTCTCTCCA 2297
QY 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTGCAACCTTAACCTGCAAGGCTTACAGAA 2220
Db 2298 GCCATCAAGCATCTGCCAGGCCAGAAACTGCAACCTTAACCTGCAAGGCTTACAGAA 2357
QY 2221 AGCATTTCTAGAGTCAACCACTGCTGTGTCCTCAAGAAAAATGTTCAAGTTGCAAG 2280
Db 2358 AGCATTTCTAGAGTCAACCACTGCTGTGTCCTCAAGAAAAATGTTCAAGTTGCAAG 2417
QY 2281 TCAATCTCAACCAAGACCGTTCTATAGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2340
Db 2418 TCAATCTCAACCAAGACCGTTCTATAGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2477
QY 2341 TTGTCTGTCTCTCCCATGAGTCCGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2400
Db 2478 TTGTCTGTCTCTCCCATGAGTCCGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2537
|||||

QY 2401 ATCAGGTCGACGAGGAACTGAATATATCAACTTTTCAGGAGGAGTCAAGTGCCTCCAGA 2460
| | | | |
Db 2538 ATAGAGTCGACCGAGGAACGTAATATACACTTTTCAGGAGGAGTCAAGTGCCTCCAGA 2597
| | | | |
QY 2461 GGCAGCCCAAGATTTTATCCCAATAGAGGAAATCCAAATTTTATTAATCTAGTAAGAG 2520
| | | | |
Db 2598 GGCAGCCCAAGATTTTATCCCAATAGAGGAAATCCAAATTTTATTAATCTAGTAAGAG 2657
| | | | |
QY 2521 GTGGGTCCCGAAGAGACAGACACACTTTTGAATGCCGACCCGACGCTGCGCAGAGGA 2580
| | | | |
Db 2658 GTGGGTCCCGAAGAGACAGACACACTTTTGAATGCCGACCCGACGCTGCGCAGAGGA 2717
| | | | |
QY 2581 GCTGCTTTTCATCAGACTCTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
| | | | |
Db 2718 GCTGCTTTTCATCAGACTCTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2777
| | | | |
QY 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATATA 2694
| | | | |
Db 2778 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATATA 2831
| | | | |

RESULT 13
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sander, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 97.4%; Score 2625.2; DB 19; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAAGTCGGGCGCGGAGAGGTCTGTGAACTCGCGACCGCGCAGAGGCG 60
| | | | |
Db 165 ATGAAGATGTGAAGTCGGGCGCGGAGAGGTCTGTGAACTCGCGACCGCGCAGAGGCG 224
| | | | |
QY 61 GACGGCTGTACTGTGCTGAGGACCCGCGCGGACAGCGTGTGAGCGCGGCTGAGCTTG 120
| | | | |
Db 225 GACGGCTGTACTGTGCTGAGGACCCGCGCGGACAGCGTGTGAGCGCGGCTGAGCTTG 284
| | | | |
QY 121 AGGGAAGCCCGCGGAGGACAGAGGGGGCCCGAGATGAGCTGCTGGGAAAGCCGCTCTCT 180
| | | | |
Db 285 AGGGAAGCCCGCGGAGGACAGAGGGGGCCCGAGATGAGCTGCTGGGAAAGCCGCTCTCT 344
| | | | |
QY 181 TACAGAGTAGCAGAGCTGCGCGGCGCAAGTCAAGTACCGGGGGTGCAGAACTACCTG 240
| | | | |
Db 345 TACAGAGTAGCAGAGCTGCGCGGCGCAAGTCAAGTACCGGGGGTGCAGAACTACCTG 404
| | | | |
QY 241 TACAAGCTGTGAGAGACCCCGCGGCTGGGCTTCACTTACCAAGCTTTGTTTTCTC 300
| | | | |

Db 405 TACAAGCTGTGAGAGACCCCGCGGCTGGGCTTCACTTACCAAGCTTTGTTTTCTC 464
| | | | |
QY 301 CTGTGCTTTGGTGGCTGATTTTTCAGATGTTTTCATACCATCCCTGAGCACAATAATG 360
| | | | |
Db 465 CTGTGCTTTGGTGGCTGATTTTTCAGATGTTTTCATACCATCCCTGAGCACAATAATG 524
| | | | |
QY 361 GCGTCAGATTTGCTCTTGAATCCGAGAGTTCGATGATTTGTCGCTTTGGTTTGAAGTTC 420
| | | | |
Db 525 GCGTCAGATTTGCTCTTGAATCCGAGAGTTCGATGATTTGTCGCTTTGGTTTGAAGTTC 584
| | | | |
QY 421 ATCATTCGATTCGGTCTGCGGGTGTGCTGTTCGATATAGAGATGGCAGAGAGACTG 480
| | | | |
Db 585 ATCATTCGATTCGGTCTGCGGGTGTGCTGTTCGATATAGAGATGGCAGAGAGACTG 644
| | | | |
QY 481 AGGTTTGCCTGGAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATPAGA 540
| | | | |
Db 645 AGGTTTGCCTGGAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATPAGA 704
| | | | |
QY 541 GTTGTTTTCGCAAAAACCTCAGGGTAATATTTTTCGACGCTGCACTCAGAACTCCGT 600
| | | | |
Db 705 GTTGTTTTCGCAAAAACCTCAGGGTAATATTTTTCGACGCTGCACTCAGAACTCCGT 764
| | | | |
QY 601 TTCTTACAGATCTCCGCAATGCTGCGCATGACCCGAGGGAGGCACTTGGAAATTAATCTG 660
| | | | |
Db 765 TTCTTACAGATCTCCGCAATGCTGCGCATGACCCGAGGGAGGCACTTGGAAATTAATCTG 824
| | | | |
QY 661 GGTTCAAGTGTATTATGCTCAGCAAGAAATTAATCAGCTGTGATACAATAGATTTTGTG 720
| | | | |
Db 825 GGTTCAAGTGTATTATGCTCAGCAAGAAATTAATCAGCTGTGATACAATAGATTTTGTG 884
| | | | |
QY 721 GTTCTTATTTTTCGCTTCTTCCCTGTATCTATCTGTGTAAGAAAGATGCAATTAAGATTT 780
| | | | |
Db 885 GTTCTTATTTTTCGCTTCTTCCCTGTATCTATCTGTGTAAGAAAGATGCAATTAAGATTT 944
| | | | |
QY 781 TCTACATATGAGATGCTCTCTGTGAGGACCAATTAATCACTTGAACAATTTGGCTATGGA 840
| | | | |
Db 945 TCTACATATGAGATGCTCTCTGTGAGGACCAATTAATCACTTGAACAATTTGGCTATGGA 1004
| | | | |
QY 841 GACAAAACCTCCCTTAACCTTGGCTGGGAAGATGCTTTCGACGAGCTTGCACCTCTGGGC 900
| | | | |
Db 1005 GACAAAACCTCCCTTAACCTTGGCTGGGAAGATGCTTTCGACGAGCTTGCACCTCTGGGC 1064
| | | | |
QY 901 ATTTCTTTTTCGACCTTCTCCCGCAATTCCTGCTCAGGTTTTCATTAAGATACAA 960
| | | | |
Db 1065 ATTTCTTTTTCGACCTTCTCCCGCAATTCCTGCTCAGGTTTTCATTAAGATACAA 1124
| | | | |
QY 961 GAAACAACCCGCGCAGAAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAATCTCATTCG 1020
| | | | |
Db 1125 GAAACAACCCGCGCAGAAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAATCTCATTCG 1184
| | | | |
QY 1021 TGTGTTTGGCGTATGTTTACGACACTGATGAGAAATCTGTTTCCATTGCAACTTGGAAAGCA 1080
| | | | |
Db 1185 TGTGTTTGGCGTATGTTTACGACACTGATGAGAAATCTGTTTCCATTGCAACTTGGAAAGCA 1244
| | | | |
QY 1081 CACTTGAAGGCTTGCACACTGACGACCTTACCAAGAAAGAAACAAGGGAGACATCAAGC 1140
| | | | |
Db 1245 CACTTGAAGGCTTGCACACTGACGACCTTACCA----- 1279
| | | | |
QY 1141 AGTCAGAACTTAAGTTTAAGAGCGAGTGCAGATGCTAGGCCCGCAGAGGCGCAGAGTAT 1200
| | | | |
Db 1280 --TCAGAACTTAAGTTTAAGAGCGAGTGCAGATGCTAGGCCCGCAGAGGCGCAGAGTAT 1337
| | | | |
QY 1201 AAGAGCCGACAAAGCTCAATAGTGAACAGAGAGTCCCAAGCAACCGACATACACCGGAG 1260
| | | | |
Db 1338 AAGAGCCGACAAAGCTCAATAGTGAACAGAGAGTCCCAAGCAACCGACATACACCGGAG 1397
| | | | |
QY 1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGACTTCAACGACCGAACCAGCTTCCGCGCC 1320
| | | | |
Db 1398 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGACTTCAACGACCGAACCAGCTTCCGCGCC 1457
| | | | |
QY 1321 TCGCTGCGCTCAAAAGTTTCTAGCCCAAAACAGTATATGATGTGACACAGCCTTGGC 1380
| | | | |
Db 1458 TCGCTGCGCTCAAAAGTTTCTAGCCCAAAACAGTATATGATGTGACACAGCCTTGGC 1517
| | | | |

QY	1381	ACTGATATGTAATGATGAAAAAGATGCCAGTGTGATGATCAAGTGAAGACCTCAC	1440
Db	1518	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTGATGATCAAGTGAAGACCTCAC	1577
QY	1441	CCACCACTTAAACGTGATCTCGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG	1500
Db	1578	CCACCACTTAAACGTGATCTCGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG	1637
QY	1501	AAGTTTAAAGAAAGGTTACGTCATATGATGTAAAAAGTGTGATTTGAACATATTTGCT	1566
Db	1638	AAGTTTAAAGAAACATTACGTCATATGATGTAAAAAGTGTGATTTGAACATATTTGCT	1697
QY	1561	GGTCATCTGACATGTTGTGTGAAATTTAAAGCCTTCAACACGTGTGATCAAAATCTT	1620
Db	1698	GGTCATCTGACATGTTGTGTGAAATTTAAAGCCTTCAACACGTGTGATCAAAATCTT	1757
QY	1621	GGAAAAGGGCAATACATCACTACGATTTAAGAAAGCCGAGAGAAATTTACACGCAAACTGAG	1680
Db	1758	GGAAAAGGGCAAAATACATCACTACGATTTAAGAAAGCCGAGAGAAATTTACACGCAAACTGAG	1817
QY	1681	ACCAACAGACGATCTCAGATGATCTCGTTCGSGTGTCAAGGTTGAAAAACAGTACAGTCC	1740
Db	1818	ACCAACAGACGATCTCAGATGATCTCGTTCGSGTGTGTGAAGAAACAGTACAGTCC	1877
QY	1741	ATGAGTTCCAAGTTGAGCTGCGCTTACTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT	1800
Db	1878	ATGAAATTCCAAGCTGAGACTGCTCTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT	1937
QY	1801	GCCACAGCCCTCGCTTTGGGCTTCACTTCAGATCCCACTTTTGAATGTGAACAACATCT	1860
Db	1938	GCCACAGCCCTCGCTTTGGGCTTCACTTCAGATCCCACTTTTGAATGTGAACAACATCT	1997
QY	1861	GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCCGACAAACACATGCGTGC	1920
Db	1998	GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCCGACAAACACATGCGTGC	2057
QY	1921	TTATCCGATCTCACTAGTCCCAACATCTCCAGAGAGCCCTGCGATTCATTTCTGACGCCAAT	1980
Db	2058	TTATCCGATCTCACTAGTCCCAACATCTCCAGAGAGCCCTGCGATTCATTTCTGACGCCAAT	2117
QY	1981	GAGTTCAGTGGCCAGACTTTTCTAGCGCGTTAGCCCTACTATGACACAGTCAAGCAACACAG	2040
Db	2118	GAGTTCAGTGGCCAGACTTTTCTAGCGCGTTAGCCCTACTATGACACAGTCAAGCAACACAG	2177
QY	2041	GTGCCAATTAAGTCAAAAGCATGAGTCTCAGACGTGCGACGCCAACCAACCATTTGCAACCAA	2100
Db	2178	GTGCCAATTAAGTCAAAAGCATGAGTCTCAGACGTGCGACGCCAACCAACCATTTGCAACCAA	2237
QY	2101	ATTAATATGCGGACGCCAAGCCAGACGCCCAACAACCTTACAGATCCCAACCTCCCTCCCA	2160
Db	2238	ATTAATATGCGGACGCCAAGCCAGACGCCCAACAACCTTACAGATCCCAACCTCCCTCCCA	2297
QY	2161	GCCATCAAGCATCTGCCCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCACAGGCTTACAGAAA	2220
Db	2298	GCCATCAAGCATCTGCCCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCACAGGCTTACAGAAA	2357
QY	2221	AGCATTTTCTGACGTGCACCACTGCGCTTGTTCCTCTCCAGAGAAATGTTCAAGTTGACACAG	2280
Db	2358	AGCATTTTCTGACGTGCACCACTGCGCTTGTTCCTCTCCAGAGAAATGTTCAAGTTGACACAG	2417
QY	2281	TCAAAATCTCAACCAAGACCGTTCTATAGAGAAAAAGCTTTGACATGTGGAGAGAAACTCTG	2340
Db	2418	TCAAAATCTCAACCAAGACCGTTCTATAGAGAAAAAGCTTTGACATGTGGAGAGAAACTCTG	2477
QY	2341	TTGTCTGTCTGTGCCATGAGTGCAGAAAGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400
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OY      2521  GTGGGTCCCGAAGACAGACAGACACATTTTGTATGCCGACCGAGCCTGCCAGGAA 2580
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OY      2681  GCGCCCTTTCATCAGACTCTTAAGGACGTGAAGGTCAGATCATTCTCAGACATTGT 2640
Db      2718  GCTGCTTTTCATCAGACTCTTAAGGACGTGAAGGTCAGATCATTCTCAGACATTGT 2777
OY      2641  AAGCAGAGAAAGTACAGATGCCCTCAGCTTCCTCATGTCAAAGTAATA 2694
Db      2778  AAGCAGAGAAAGTACAGATGCCCTCAGCTTCCTCATGTCAAAGTAATA 2831

RESULT 14
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
GENERAL INFORMATION:
APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
APPLICANT: Galvin, Katherine M.
APPLICANT: Healy, Aileen
APPLICANT: Acton, Susan L.
APPLICANT: Donoghue, Mary
APPLICANT: Scagliano, Nancy
APPLICANT: Perodin, Jacqueline
APPLICANT: Rodrigue-Way, Amelie
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395
TITLE OF INVENTION: 29002, 32316, 43726, 68292, 26156, 32427, 2402, 7747, 1720
TITLE OF INVENTION: 9151, 60481, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
FILE REFERENCE: MP102-018P1RNONIM
CURRENT APPLICATION NUMBER: US/10/353,690
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: 60/353,224
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/364,529
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/373,861
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: 60/388,080
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: 60/390,971
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/394,130
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/394,797
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: 60/404,904
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/405,450
PRIOR FILING DATE: 2002-08-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 2335
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-353-690-55

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Best Local Similarity 60.1%; Pred. No. 2,4e-148;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

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Qy 277 ATCTACACGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 336
Db 380 GTCTACACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 439
Qy 337 ACCATCCCTGAGCACAACAAATGGCTCAAGTTCCTCTCTCTCTCTCTCTCTCTCTCT 396
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Qy 577 ACCTCTGCACTCAGAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 636
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Db 800 ACCGCTGTGATACATCGGGTCTCTGCTGCTCATCTTGCTCTCTCTCTCTCTCTCTCT 859
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Db 1160 GCTTACCTGACGACCTGTGCTACTGATGACAGATCTCTCCATCTTTCAAGAGCTG 1219
Qy 1108 CCAACCAAGAAAGAACAGAGGGAAGCATCAAGAGTCAAGAGTA----- 1152
Db 1220 GCCCTCTTGTGAGACGTGCAACGGGCGCGCAATGGGGCTTACGGCCCTCGAGGCTG 1279
Qy 1153 ----- 1152
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Qy 1153 -----AGTTTAAAGAGCGA 1167

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Db 1340 CGCGCGGAGACGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1399
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Qy 1222 GGTGACAGGAGTCCCCCAAGACCCGACATCAGACCGGAGG---GCATGCCAACAAAGT 1278
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Db 1520 CAABAAGCTGAGAGCTTCAATGACCGACCCGCTTCCGGGCACTCTGAGAGT----- 1573
Qy 1339 TCTCAGCCAAAACCAAGTATGATGCTGACAGACCCCTTGGGCACTGATATATATGAT 1398
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Qy 1579 TGTAGAAATTAAGAAAGCTTCAAAACAGTGTGATCAAACTTTGGAAGAAAGGCG---AAATC 1635
Db 1802 GCGCGGATCAAGAGCTTGAAGAACTGGGTGACCAATTTGGGTGGGGGCGCGGAGAC 1861
Qy 1636 ACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAGACCAAGACATCTC 1695
Db 1862 AGGAAGGCGCGGAGAGAGGCGCAGCAAGGGGCGCTCCGAGCGGAGGTGTGATGAATC 1921
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Qy 1876 GTGATAGCAAAAGATCTTTCGGGTTCCGACAAA 1909
Db 2096 GTGACCAAGAGACATCTCTCTCCGACAGA 2129

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RESULT 15
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
FEATURE:
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-10-850-928-1

Query Match 19.2%; Score 518.4; DB 21; Length 2335;
Best Local Similarity 60.1%; Pred. No. 2.4e-148;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

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1982 GACTG 2035
1816 TTGCTTCAATTCAGATCCACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1875
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Job time : 1392.19 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:19:35 ; Search time 293.522 Seconds
(without alignments)
14867.549 Million cell updates/sec

Title: US-09-810-796-3

Perfect score: 2667

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2662.2	99.8	3111	4	US-09-825-147-3
3	2625.2	98.4	3137	4	US-09-590-304-1
4	2617.2	98.1	3074	4	US-09-813-148-1
5	509.8	19.1	582	4	US-09-495-050A-303
6	492	18.4	2196	4	US-09-949-016-1823
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8	489.2	18.3	2273	3	US-09-177-650-88
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20	363.8	13.6	930	3	US-09-105-058C-17
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37	266.6	10.0	2821	4	US-09-949-016-32	Sequence 32, App
38	266.6	10.0	2821	4	US-09-949-016-32	Sequence 32, App
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41	134.6	5.0	251	3	US-09-495-050A-296	Sequence 296, App
42	95.8	3.6	171	3	US-09-177-650-102	Sequence 102, App
43	95.8	3.6	58543	4	US-09-949-016-13565	Sequence 13565, App
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45	84.8	3.2	649	3	US-09-177-650-118	Sequence 118, App

ALIGNMENTS

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RESULT 1
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 106 ATGAAGATGTGAGTGTGGCGCGGCGGAGGCTGTGCTGAATCGGACCGCCAGGGGC 165
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QY 361 GCCTCAAGTTGCTCTTGTGATCTGAGATTCGTGATGATTTGTGCTTTTGGAGTTTC 420
Db 466 GCCTCAAGTTGCTCTTGTGATCTGAGATTCGTGATGATTTGTGCTTTTGGAGTTTC 525
QY 421 ATCATTCGATCGATCGTCTGAGGATGCTGTGTGATATAGAGGATGGAGAGAACTG 480
Db 526 ATCATTCGATCTGATCTGAGGATGCTGTGTGATATAGAGATGGAGAGAACTG 585
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTTATCCCTTCAATAGCA 540
Db 586 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTTATCCCTTCAATAGCA 645
QY 541 GTTGTCTTCTGCAAAAACCTGAGGATATATTTTGGCACTGTGCACTCAAGAGTCCGT 600
Db 646 GTTGTCTTCTGCAAAAACCTGAGGATATATTTTGGCACTGTGCACTCAAGAGTCCGT 705
QY 601 TTCTCTACAGATCCCTCCGATGGTGGCATGGACCGAAGGGAGGCACTTGGAAATTACTG 660
Db 706 TTCTCTACAGATCCCTCCGATGGTGGCATGGACCGAAGGGAGGCACTTGGAAATTACTG 765
QY 661 GGTTCAGTGTATATGCTCAACAGCAAGAAATTAATCAGAGCTTGTATAGATATTTTGG 720
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QY 721 GTTCTTATTTTTCGTCTTCTCTGTCTATCTGTGTGAAAAGAGATGCCAATTAAGATT 780
Db 826 GTTCTTATTTTTCGTCTTCTCTGTCTATCTGTGTGAAAAGAGATGCCAATTAAGATT 885
QY 781 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATGCACTATGAGCTATAGGA 840
Db 886 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATGCACTATGAGCTATAGGA 945
QY 841 GACAAAACCTCCCTTAACTTGTGGGAGAGATTGCTTTTGCAGAGCTTTTGCACCTCTTGGC 900
Db 946 GACAAAACCTCCCTTAACTTGTGGGAGAGATTGCTTTTGCAGAGCTTTTGCACCTCTTGGC 1005
QY 901 ATTTCTTTCTTTGCACTTCTGTGCGGCAATTTTGGCTCAGGTTTGTGCAATTAAGTACA 960
Db 1006 ATTTCTTTCTTTGCACTTCTGTGCGGCAATTTTGGCTCAGGTTTGTGCAATTAAGTACA 1065
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Db 1066 GAACAAACCGGCGAGAAACATTTTGAAGAAAGAGAACCCAGCTGCCAACTCAATTGAG 1125
QY 1021 TGTGTTTGGCGTATGTTACGCACTGATGAGAAATCTGTTTCAATTGCAACTTGGAAGCCA 1080
Db 1126 TGTGTTTGGCGTATGTTACGCACTGATGAGAAATCTGTTTCAATTGCAACTTGGAAGCCA 1185
QY 1081 CACTTGAAGGCTTGTGACACCTGTGAGCCCTTACCAATCAGAAAGTATTTTAAAGAGGA 1140
Db 1186 CACTTGAAGGCTTGTGACACCTGTGAGCCCTTACCAATCAGAAAGTATTTTAAAGAGGA 1245
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QY 1201 AGAAGGTCCCAAGACCGCATCAACGCGAGGGAGTCCCAACAAAGTGCAGAAAGAC 1260
Db 1306 AGAAGGTCCCAAGACCGCATCAACGCGAGGGAGTCCCAACAAAGTGCAGAAAGAC 1365
QY 1261 TGGAGTTTCAAGACCGGAACCCGCTTCCGGCCCTGCTGTGCTCAAAAGTCTCAGCCA 1320
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QY 1321 AAACCATGATATGCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA 1380
Db 1426 AAACCATGATATGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGA 1485

QY 1381 TGCCAGTGTGATGTATCAGTGGAGAACCTCACCCACCACCTTAAACTGTCAATGAGCT 1440
Db 1486 TGCCAGTGTGATGTATCAGTGGAGAACCTCACCCACCACCTTAAACTGTCAATGAGCT 1545
QY 1441 ATCAGAAATTAAGAAATTTTCAATGTTGGCAAAACGGAAGTTTAAAGAAACCTTACGTCATAT 1500
Db 1546 ATCAGAAATTAAGAAATTTTCAATGTTGGCAAAACGGAAGTTTAAAGAAACCTTACGTCATAT 1605
QY 1501 GATGTAAAGATGTGATTTGAAACAATATTTCTGTGGTCACTGTGAGACATGTTGTGAAATT 1560
Db 1606 GATGTAAAGATGTGATTTGAAACAATATTTCTGTGGTCACTGTGAGACATGTTGTGAAATT 1665
QY 1561 AAAAGCCTTCAAAACAGTGTGATCAAAATTTTGGAAAAAGGCAAAATCACAATCAGATAG 1620
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QY 1681 CGGGTGTCAAGGTTGAAAAAAGGTAAGTCAATAGATGCAAGCTGGAAGCTGCTACTA 1740
Db 1786 CGGGTGTCAAGGTTGAAAAAAGGTAAGTCAATAGATGCAAGCTGGAAGCTGCTACTA 1845
QY 1741 GACATCTATCAACAGGTCCTTTCGAAAAGGCTCTGCTCAGCCCTGCTTGGCTTCAATTC 1800
Db 1846 GACATCTATCAACAGGTCCTTTCGAAAAGGCTCTGCTCAGCCCTGCTTGGCTTCAATTC 1905
QY 1801 CAGATCCCACTTTTGAATGTGGAACAGACATCTGACTATCAAAAGCCCTGTGATATGCAAA 1860
Db 1906 CAGATCCCACTTTTGAATGTGGAACAGACATCTGACTATCAAAAGCCCTGTGATATGCAAA 1965
QY 1861 GATCTTTGGGTTCCGCAAAAACAGTGGCTGCTTATCAGATCAACTAGTGGCAACATTC 1920
Db 1966 GATCTTTGGGTTCCGCAAAAACAGTGGCTGCTTATCAGATCAACTAGTGGCAACATTC 2025
QY 1921 TCGAAGGCTGTGCAAGTTCAATTTCTGACCGCAAAATGATCAGTGCCCAAGCTTTTCAAGCG 1980
Db 2026 TCGAAGGCTGTGCAAGTTCAATTTCTGACCGCAAAATGATCAGTGCCCAAGCTTTTCAAGCG 2085
QY 1981 CTTAGCCCTTACTATATGACAGTCAAGCAACACAGGTGCCAATTAAGTCAAAAGGATGCTCA 2040
Db 2086 CTTAGCCCTTACTATATGACAGTCAAGCAACACAGGTGCCAATTAAGTCAAAAGGATGCTCA 2145
QY 2041 GCAGTGGCAGCCACCAACACACCATTTGCCAAACCAATTAATTAAGGCAACCCAGCAGACC 2100
Db 2146 GCAGTGGCAGCCACCAACACACCATTTGCCAAACCAATTAATTAAGGCAACCCAGCAGACC 2205
QY 2101 CCAACCACTTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATTTGCCAGGCGAGAA 2160
Db 2206 CCAACCACTTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATTTGCCAGGCGAGAA 2265
QY 2161 ACTCTGCAACCCCTTAAACCTGTGAGGCTTACAGAAAGCATTTTGTGACGTCACCACTGCTTT 2220
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QY 2341 GACTTGGGCAAAATCTTTGTCTGTGCAAAAACCTGATCAGTGTGACCGAGGAACCTGAATATA 2400
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Db 2506 CAACCTTTCAGGAGATGATGCAAGTGGCTCCAGAGGACCAAGATTTTTCACCAAAATTG 2565
QY 2461 AGGAATTCAAAATTTGTTTATTAATGATGAAGAGGTGGGTCCGGAAGAGACAGAGACAGAC 2520

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Db 2566 AGGAATCCAAATGTTTATPACATGATGAAGAGGTGGTCCCGAAGAGACAGACGAC 2625
Qy 2521 ACTTTTATGCGCGACCGGACGCTGCGACGGAAGCTGCTTTGATCAGACTCTTAAG 2580
Db 2626 ACTTTTATGCGCGACCGGACGCTGCGACGGAAGCTGCTTTGATCAGACTCTTAAG 2685
Qy 2581 ACTGAAGTCAAGCATCATCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2640
Db 2686 ACTGAAGTCAAGCATCATCAGAGCATTTGTAAAGCAGAGAAAGTACAGATGCCCTC 2745
Qy 2641 AGCTTGCTCATGTCAAACTGAATAA 2667
Db 2746 AGCTTGCTCATGTCAAACTGAATAA 2772

RESULT 2
US-09-825-147-3
Sequence 3, Application US/09825147
Patent No. 6767736
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedlich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sandu, Arthur T.
TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
FILE REFERENCE: LEX-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
CURRENT FILING DATE: 2001-04-03
PRIORITY FILING DATE: 2000-04-03
PRIORITY FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Faeseq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-3

Query Match 99.8%; Score 2662.2; DB 4; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAAGATGTGAGTGTGGGCGGCGGCGAGGCTGCTGTAAGTCTGCGAGCGCGCGAGGCG 60
Db 165 ATGAAGATGTGAGTGTGGGCGGCGGCGAGGCTGCTGTAAGTCTGCGAGCGCGCGAGGCG 224
Qy 61 GACGGCTGCTGTAAGTGTGGGCGGCGGCGCGAGGCTGCTGTAAGTCTGCGAGCGCGAGGCG 120
Db 225 GACGGCTGCTGTAAGTGTGGGCGGCGGCGCGAGGCTGCTGTAAGTCTGCGAGCGCGAGGCG 284
Qy 121 AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180
Db 285 AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 344
Qy 181 TACACGATGACGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 345 TACACGATGACGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 404
Qy 241 TACACGATGACGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 405 TACACGATGACGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 464
Qy 301 CTGTGCTTTGGTGTGATTTGTGATGTTTCTAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 360
Db 465 CTGTGCTTTGGTGTGATTTGTGATGTTTCTAAGTCTTCTAAGTCTTCTAAGTCTTCTAAGTCTT 524
Qy 361 GCCTCAAGTTGCTCTTGAATCTGAGATTCGTGATGATGATGATGATGATGATGATGATGATGAT 420
|||||

Db 525 GCCTCAAGTTGCTCTTGAATCTGAGATTCGTGATGATGATGATGATGATGATGATGATGATGAT 584
Qy 421 ATCATTCGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 585 ATCATTCGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 644
Qy 481 AGGTTGCTGCAAGGCGCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 645 AGGTTGCTGCAAGGCGCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 704
Qy 541 GTTGTGCTGCAAGGCGCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 705 GTTGTGCTGCAAGGCGCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 764
Qy 601 TTCTCAAGATCTCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 765 TTCTCAAGATCTCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 824
Qy 661 GGTTCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 825 GGTTCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 884
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Db 885 GTTCTTAATTTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 944
Qy 781 TCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 945 TCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
Qy 841 GACAAACTCCCTTAATCTGCTGAGGAGATGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAG 900
Db 1005 GACAAACTCCCTTAATCTGCTGAGGAGATGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAG 1064
Qy 901 ATTTCTTTCTTCTGACCTTCTGCGGCAATCTTGTGCTGAGGCTTCTGAGGCTTCTGAGGCTTCT 960
Db 1065 ATTTCTTTCTTCTGACCTTCTGCGGCAATCTTGTGCTGAGGCTTCTGAGGCTTCTGAGGCTTCT 1124
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Qy 1021 TGTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1185 TGTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1244
Qy 1081 CACTTAAGGCTTGTGACACTGACGCTTACCAATCAGAGCTTAAGTTTAAAGAGCA 1140
Db 1245 CACTTAAGGCTTGTGACACTGACGCTTACCAATCAGAGCTTAAGTTTAAAGAGCA 1304
Qy 1141 GTGCGAT 1200
Db 1305 GTGCGAT 1364
Qy 1201 AGGAGGTCCCGCAAGCAGCAATCAAGCGAGGAGTCCCAAGGTGAGAGAGC 1260
Db 1365 AGGAGGTCCCGCAAGCAGCAATCAAGCGAGGAGTCCCAAGGTGAGAGAGC 1424
Qy 1261 TGAAGCTTCAAGCAGCAAGCAGCAGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1425 TGAAGCTTCAAGCAGCAGCAGCAGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1484
Qy 1321 AAACGAT 1380
Db 1485 AAACGAT 1544
Qy 1381 TGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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Qy 1441 ATCAGATTAATGAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1605 ATCAGATTAATGAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1664
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QY 1501 GATGTAAGATGTCATTGTAACAATATTTCTGTGTGATCTGACATGTGTGTAGAAAT 1560
DB 1665 GATGTAAAGATGTCATTGTAACAATATTTCTGTGTGATCTGACATGTGTGTAGAAAT 1724
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DB 1725 AAAAGCCTTAAACAGGTGTTGATCAAAATCTTGAAAAAGGCAAAATCACATCAGATAAG 1784
QY 1621 AAGAGCCGAGAGAAATTAACAGCAGAACATGAGACCAAGACGATCTCAGTATGCTCGGT 1680
DB 1785 AAGAGCCGAGAGAAATTAACAGCAGAACATGAGACCAAGACGATCTCAGTATGCTCGGT 1844
QY 1681 CGGTGTGTCAGAGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGACCTCTACTA 1740
DB 1845 CGGTGTGTCAGAGTTGAAAAACAGGTACAGTCCATAGAAATCCAAAGCTGAGCTCTACTA 1904
QY 1741 GATATCTATCAACAGTCTCTTCCGAAAAAGCTGTGCTCAGCTCTCGCTTTGGCTTATTC 1800
DB 1905 GACATCTATCAACAGTCTCTTCCGAAAAAGCTGTGCTCAGCTCTCGCTTTGGCTTATTC 1964
QY 1801 CAGATCCCACTTTGTAATGTGAACAGACATCTGACTATCAAAAGCCTGTGTGATAGCAAA 1860
DB 1965 CAGATCCCACTTTGTAATGTGAACAGACATCTGACTATCAAAAGCCTGTGTGATAGCAAA 2024
QY 1861 GATCTTTCCGGGTTCCGCACAAAAACAGTGTGCTGTTATCCAGATCAACTAGTCCCAATC 1920
DB 2025 GATCTTTCCGGGTTCCGCACAAAAACAGTGTGCTGTTATCCAGATCAACTAGTCCCAATC 2084
QY 1921 TCGAGAGGCTCGAGTTCATTCTGAGCCGAAAAAGATTCAGTGCCCAAGCTTTCTACGGG 1980
DB 2085 TCGAGAGGCTCGAGTTCATTCTGAGCCGAAAAAGATTCAGTGCCCAAGCTTTCTACGGG 2144
QY 1981 CTTAGCCCTTACTATGACAGTCAAGCAACAAGGTCCCAATTAGTCAAAAGCATGAGCTCA 2040
DB 2145 CTTAGCCCTTACTATGACAGTCAAGCAACAAGGTCCCAATTAGTCAAAAGCATGAGCTCA 2204
QY 2041 GCAGTGGCAGCCACCAACCAATTCGCAAAACAAATTAATACGGCACCCAAAGCAGAGCC 2100
DB 2205 GCAGTGGCAGCCACCAACCAATTCGCAAAACAAATTAATACGGCACCCAAAGCAGAGCC 2264
QY 2101 CCAACAACTTTACAGATCCCACTCTCTCCCAAGCATCAAGATTTGGCCAGGCGCAAGAA 2160
DB 2265 CCAACAACTTTACAGATCCCACTCTCTCCCAAGCATCAAGATTTGGCCAGGCGCAAGAA 2324
QY 2161 ACTCTGACCCCTTAACCTGCAAGCTTACAGAAAGCATTTCTGACGTCAACCTGCTCT 2220
DB 2325 ACTCTGACCCCTTAACCTGCAAGCTTACAGAAAGCATTTCTGACGTCAACCTGCTCT 2384
QY 2221 GTTGCTCTCAAGAAAAATGTTCAAGTTGCAAGTCAAAATCTCAACAAAGACCGTTCTATG 2280
DB 2385 GTTGCTCTCAAGAAAAATGTTCAAGTTGCAAGTCAAAATCTCAACAAAGACCGTTCTATG 2444
QY 2281 AAGAAAAAGCTTTGACATGGAAGAGAAACCTGCTGTCTGTCTGCTCCCATGTGTCCGAAG 2340
DB 2445 AAGAAAAAGCTTTGACATGGAAGAGAAACCTGCTGTCTGTCTGTCTCCCATGTGTCCGAAG 2504
QY 2341 GACTTGGGCAAAATCTTTGTCTGTGCAAAAACCTGATCAGGTGCAACGAGAACTGAATATA 2400
DB 2505 GACTTGGGCAAAATCTTTGTCTGTGCAAAAACCTGATCAGGTGCAACGAGAACTGAATATA 2564
QY 2401 CAACCTTTCAAGGAGTGAAGTGAAGTGTGCTCAAGAGCAGCCAAAGATTTTAACTCCCAATGG 2460
DB 2565 CAACCTTTCAAGGAGTGAAGTGAAGTGTGCTCAAGAGCAGCCAAAGATTTTAACTCCCAATGG 2624
QY 2461 AAGGAATCAAAATGTTTATTAATCTGATGAAGAGTGTGTCCGGAAGAGACAAAGACAGAC 2520
DB 2625 AAGGAATCAAAATGTTTATTAATCTGATGAAGAGTGTGTCCGGAAGAGACAAAGACAGAC 2684
QY 2521 ACTTTTGTATGCGCAACCGAGCTGTCCAGGAAAGTGTCTTTGACATCAGACTCTTAAGG 2580
DB 2685 ACTTTTGTATGCGCAACCGAGCTGTCCAGGAAAGTGTCTTTGACATCAGACTCTTAAGG 2744

QY 2581 ACTGGAAGTCAAGATCATCTCAGAGCAATTTGTAAAGGAGAAAGTACAGATGCCCTC 2640
DB 2745 ACTGGAAGTCAAGATCATCTCAGAGCAATTTGTAAAGGAGAAAGTACAGATGCCCTC 2804
QY 2641 AGCTTGCTCATGTCAAACTGAATTA 2667
DB 2805 AGCTTGCTCATGTCAAACTGAATTA 2831

RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTCCGGCCGGGCGAGGTGCTGCTGAATCGGCAAGCCGCGAGGCG 60
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DB 61 GACGGCTGTACTACTGCTGGGCAACCGCGGCGCAAGCTTGTGTGGCGGCGGCTGGCTG 120
QY 121 AGGAGAGCCCGCGGGGCAAGCGGGGCGCGATGAGCTTGTGGGAAAGCCGCTCT 180
DB 121 AGGAGAGCCCGCGGGGCAAGCGGGGCGCGATGAGCTTGTGGGAAAGCCGCTCT 180
QY 181 TACAGGATAGCCAGAGCTGCGCGGCAAGCTCAAGTACCGGCGGTCAGAACTAAGCTG 240
DB 181 TACAGGATAGCCAGAGCTGCGCGGCAAGCTCAAGTACCGGCGGTCAGAACTAAGCTG 240
QY 241 TACAAGTGTGAGAGAACCCCGGCGCTGGGCTTCATCTCAACGCTTGTGTTTCTC 300
DB 241 TACAAGTGTGAGAGAACCCCGGCGCTGGGCTTCATCTCAACGCTTGTGTTTCTC 300
QY 301 CTGTCTTTGTTGCTTGAATTTTGTCAAGTGTTCATCTCAACGCTTGTGTTTCTC 360
DB 301 CTGTCTTTGTTGCTTGAATTTTGTCAAGTGTTCATCTCAACGCTTGTGTTTCTC 360
QY 361 GCTCAAGTGTGCTTGAATCTGAGTGTGAGTGTGAGTGTGCTTGTGTTGAGTTT 420
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QY 421 ATCAATTCGAATCTGTGCTGCGGTTGTGTGATTAAGAGATGGCAAGAAAGCTG 480
DB 421 ATCAATTCGAATCTGTGCTGCGGTTGTGTGATTAAGAGATGGCAAGAAAGCTG 480
QY 481 AGTTTGTCTGAAGACCCCTTCTGTGTTAAGATACCAATGTTCTTATCGCTTCAATACGA 540
DB 481 AGTTTGTCTGAAGACCCCTTCTGTGTTAAGATACCAATGTTCTTATCGCTTCAATACGA 540
QY 541 GTTGTTTCTGAAGAAACCTCAAGGTTAATTTTTCACAGTGTGCACTCAGAAAGTCTCGGT 600
DB 541 GTTGTTTCTGAAGAAACCTCAAGGTTAATTTTTCACAGTGTGCACTCAGAAAGTCTCGGT 600

QY 601 TTCTACAGATCCCTCGCATGTGCGCATGSAACGAGGGGAGCACTTGGAAATTACTG 660
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Db 601 TTCTACAGATCCCTCGCATGTGCGCATGSAACGAGGGGAGCACTTGGAAATTACTG 660
QY 661 GGTTCAGTGGTTATGCTCAACAGAGAAATTAAATCAAGCTTGGTATCATAGATTTTGG 720
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Db 661 GGTTCAGTGGTTATGCTCAACAGAGAAATTAAATCAAGCTTGGTATCATAGATTTTGG 720
QY 721 GTTCTTATTTTTCGCTCTTCTTCTTCTATCTGGTGGAAAAAGATGGCAATTAAGATT 780
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Db 781 TCTACATATGACAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTTATGGCTATGA 840
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Db 841 GACAAAATCTCCCTTAATCTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTCGACTTCCTGGC 900
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Db 901 ATTTCTTTCTTTGACATTTCTGCGCGGCACTTCTGGCTCAGGTTTGGATTTAAAGTCA 960
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Db 961 GAACAACACCGCCAGAAACATTTGAGAAAGAAAGAACCCAGCTGCCAATCTCATTCAG 1020
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Db 1021 TGTGTTTGGCGTATGACGAGCTGATGAGAAATCTGTTTCAATTGCACTTGGAAAGCCA 1080
QY 1081 CACTTGAAGGCTTGGACACCTGACAGCCCTTACCAA----- 1115
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Db 1081 CACTTGAAGGCTTGGACACCTGACAGCCCTTACCAA----- 1115
QY 1116 --TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCGCATGGCTAGCCCGAGGGCCAGAGTAT 1173
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QY 1174 AAGAGCGCAAGCGCTCAGTATGATGACAGAGGTCCCAAGCAACCAATCAGAGCCGAG 1233
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Db 1174 AAGAGCGCAAGCGCTCAGTATGATGACAGAGGTCCCAAGCAACCAATCAGAGCCGAG 1233
QY 1234 GGCAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAATCCGCTTCCGCCC 1293
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Db 1234 GGCAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAATCCGCTTCCGCCC 1293
QY 1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAATCCGCTTCCGCCC 1320
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Db 1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGAGCTTCAACGACCGAATCCGCTTCCGCCC 1320
QY 1294 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGACAGGCTTGGC 1353
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Db 1294 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGACAGGCTTGGC 1353
QY 1321 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGACAGGCTTGGC 1380
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Db 1321 TCGCTGCGCTCAAAAGTTCTCAGCCCAAAACAGTGAATGATGCTGACAGGCTTGGC 1380
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Db 1354 ACTGATGATGATATGATGAAAAAGATGCGCAGTGTGATGATCAGTGAAGAAGCTTACC 1413
QY 1381 ACTGATGATGATATGATGAAAAAGATGCGCAGTGTGATGATCAGTGAAGAAGCTTACC 1440
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Db 1381 ACTGATGATGATATGATGAAAAAGATGCGCAGTGTGATGATCAGTGAAGAAGCTTACC 1440
QY 1414 CCACCACTTAAACTGTCATTTGAGCTATCAGAAATTAAGAAATTTTCATGTTGCAAAACGG 1500
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|
Db 1414 CCACCACTTAAACTGTCATTTGAGCTATCAGAAATTAAGAAATTTTCATGTTGCAAAACGG 1500
QY 1474 AAGTTTAAAGAAAGTTAGCTTCAATATGATGATGATGATGATGATGATGATGATGATG 1533
|
|
|
Db 1474 AAGTTTAAAGAAAGTTAGCTTCAATATGATGATGATGATGATGATGATGATGATGATG 1533
QY 1501 AAGTTTAAAGAAAGTTAGCTTCAATATGATGATGATGATGATGATGATGATGATGATG 1560
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Db 1501 AAGTTTAAAGAAAGTTAGCTTCAATATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1534 GGTTCATCTGACATGTTGTGTAGAAATTAAGAGCTTCAAAACAGCTGTGATCAAAATTCCT 1593
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Db 1534 GGTTCATCTGACATGTTGTGTAGAAATTAAGAGCTTCAAAACAGCTGTGATCAAAATTCCT 1593
QY 1561 GGTTCATCTGACATGTTGTGTAGAAATTAAGAGCTTCAAAACAGCTGTGATCAAAATTCCT 1620
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Db 1561 GGTTCATCTGACATGTTGTGTAGAAATTAAGAGCTTCAAAACAGCTGTGATCAAAATTCCT 1620
QY 1594 GGAAGAGGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1653
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Db 1594 GGAAGAGGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1653
QY 1621 GGAAGAGGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1680
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Db 1621 GGAAGAGGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1680

QY 1654 ACCACAGACGATCTCAGTATGCTCGGTCCGGTGTCAAGTTGAAAAACAGTACAGTCC 1713
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Db 1681 ACCACAGACGATCTCAGTATGCTCGGTCCGGTGTCAAGTTGAAAAACAGTACAGTCC 1740
QY 1714 ATAGAGTCCAGCTGAGTGCCTTCTAGACATCTATCAACAGTCTCTTGGAAAGCTCT 1773
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Db 1741 ATAGAGTCCAGCTGAGTGCCTTCTAGACATCTATCAACAGTCTCTTGGAAAGCTCT 1800
QY 1774 GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTGAAATGTAAGACAGATCT 1833
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Db 1801 GCTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTGAAATGTAAGACAGATCT 1860
QY 1834 GACTATCAAGCCCTGAGTATGACAAAGATCTTTCCGGTTCGCAAAAACAGTGTCTG 1893
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|
|
Db 1861 GACTATCAAGCCCTGAGTATGACAAAGATCTTTGGGTTCCGCAAAAACAGTGTCTG 1920
QY 1894 TTATCCAGATCAATGATGCAATCTGAGAGGCTTGAAGTTCAATTCTGACCCAAAT 1953
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Db 1921 TTATCCAGATCAATGATGCAATCTGAGAGGCTTGAAGTTCAATTCTGACCCAAAT 1980
QY 1954 GAGTTCAGTCCGAGCTTTCTAGCGGCTTAAAGCCCTACTATGACAGTCAAGCAACAG 2013
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Db 1981 GAGTTCAGTCCGAGCTTTCTAGCGGCTTAAAGCCCTACTATGACAGTCAAGCAACAG 2040
QY 2014 GTGCCAATTATGTCAAAGCGATGGCTCAGAGTGGCAGCCACCAACCAATTCGAAACCA 2073
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Db 2041 GTGCCAATTATGTCAAAGCGATGGCTCAGAGTGGCAGCCACCAACCAATTCGAAACCA 2100
QY 2074 ATTAATACGACCAACCAAGCCAGCAAGCCCAACCACTTAAAGATCCACCTCTCTCCA 2133
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|
|
Db 2101 ATTAATACGACCAACCAAGCCAGCAAGCCCAACCACTTAAAGATCCACCTCTCTCCA 2160
QY 2134 GCCATGAACGATCTGCGCCAGGCGCAAGAACTGACACCCCAACCCCTGACAGCTTACAGGAA 2193
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|
|
Db 2161 GCCATGAACGATCTGCGCCAGGCGCAAGAACTGACACCCCAACCCCTGACAGCTTACAGGAA 2220
QY 2194 AGCATTTCTGACGTCACCACTGCTTGTGCTCCCAAGAAATGTTCAAGTTGACAG 2253
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|
Db 2221 AGCATTTCTGACGTCACCACTGCTTGTGCTCCCAAGAAATGTTCAAGTTGACAG 2280
QY 2254 TCAAATCTCAACCAAGGACGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2313
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|
Db 2281 TCAAATCTCAACCAAGGACGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2340
QY 2314 TTGTCGTCTGTCCTCACTGTCGCGAAGAGCTTGGGGAATCTTTGCTGTCGCAAAACCTG 2373
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Db 2341 TTGTCGTCTGTCCTCACTGTCGCGAAGAGCTTGGGGAATCTTTGCTGTCGCAAAACCTG 2400
QY 2374 ATCAGGTGCAACGAGGAATGAATATCAACTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2433
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Db 2401 ATCAGGTGCAACGAGGAATGAATATCAACTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2460
QY 2434 GGCAGCCAAAGTTTAACTCCCAATGAGAGGAATCCAAATGTTTAACTGATGAAGAG 2493
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Db 2461 GGCAGCCAAAGTTTAACTCCCAATGAGAGGAATCCAAATGTTTAACTGATGAAGAG 2520
QY 2494 GTGGGTCGCGAAGAGCAAGACAGCACTTTTGAATGAGCCGACCCGAGGCTCCAGGGAA 2553
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Db 2521 GTGGGTCGCGAAGAGCAAGACAGCACTTTTGAATGAGCCGACCCGAGGCTCCAGGGAA 2580
QY 2554 GCTGCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGATCTCAGAGCAATTTGT 2613
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|
|
Db 2581 GCTGCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGATCTCAGAGCAATTTGT 2640
QY 2614 AAGGCGAGGAAAGTACAGATGCTCAGCTTGGCTCATGTCAAACTGAAATPA 2667
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|
|
Db 2641 AAGGCGAGGAAAGTACAGATGCTCAGCTTGGCTCATGTCAAACTGAAATPA 2694

RESULT 4
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131

GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHER, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEEBOHM, Guiscard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF CEN
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 98.1%; Score 2617.2; DB 4; Length 3074;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

QY 1 ATGAAAGATGTGAGTCGGGCGCGGCGAGGTCGTGAACTCGGACCGCCGACGGGC 60
DB 215 ATGAAAGATGTGAGTCGGGCGCGGCGAGGTCGTGAACTCGGACCGCCGACGGGC 274
QY 61 GACGGCTCTACTGCTGGGACCCCGCGGCCACCCCTTGTTGGCGCGCGGTCCTG 120
DB 275 GACGGCTCTACTGCTGGGACCCCGCGGCCACCCCTTGTTGGCGCGCGGTCCTG 334
QY 121 AGGAGAGCGCGCGGCGGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGCTCT 180
DB 335 AGGAGAGCGCGCGGCGGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGCTCT 394
QY 181 TACACAGTAGGCGAGAGTCGCGGCGCAAGTCAGATCCGGCGGGTGCAAGTACTG 240
DB 395 TACACAGTAGGCGAGAGTCGCGGCGCAAGTCAGATCCGGCGGGTGCAAGTACTG 454
QY 241 TACACAGTCGTGAGAGACCCCGCGGCTGGCGCTTATCTACAGCTTCTGTTTCTC 300
DB 455 TACACAGTCGTGAGAGACCCCGCGGCTGGCGCTTATCTACAGCTTCTGTTTCTC 514
QY 301 CTGTCCTTGGTGTGCTGATTTTGTCAAGTCTTCTACATCCCTGAGCACAATAATG 360
DB 515 CTGTCCTTGGTGTGCTGATTTTGTCAAGTCTTCTACATCCCTGAGCACAATAATG 574
QY 361 GCGTCAGATGCTCTTGAATCTGAGATTCGATGATTTGCTTTGGTGGAGTTC 420
DB 575 GCGTCAGATGCTCTTGAATCTGAGATTCGATGATTTGCTTTGGTGGAGTTC 634
QY 421 ATCATTCGAATCGTCTGCGGGTCTGTTGCTGATTAAGAGATGCGAAGAACTG 480
DB 635 ATCATTCGAATCGTCTGCGGGTCTGTTGCTGATTAAGAGATGCGAAGAACTG 694
QY 481 AGGTTGCTGGAAGCCCTTGTGTTATAGATACATGTTCTTAATGCTTCAATAGCA 540
DB 695 AGGTTGCTGGAAGCCCTTGTGTTATAGATACATGTTCTTAATGCTTCAATAGCA 754
QY 541 GTTGTTCCTGCAAAAATCAGGGTAATATTTTGCACGCTGCACTCAGAACTCCGT 600
DB 755 GTTGTTCCTGCAAAAATCAGGGTAATATTTTGCACGCTGCACTCAGAACTCCGT 814
QY 601 TTCCTACAGATCTCGGATGCTGCGATGAGACCGAAGGGAGGCACTTTGAAATTA 660
DB 815 TTCCTACAGATCTCGGATGCTGCGATGAGACCGAAGGGAGGCACTTTGAAATTA 874
QY 661 GGTTGAGTGTATGCTCAGACGAAGAAATTAATCAGAGCTTGGTACATAGATTTT 720

DB 875 GGTTGAGTGTATGCTCAGACGAAGAAATTAATCAGAGCTTGGTACATAGATTTT 934
QY 721 GTTCTTATTTTTCGCTCTTCTTCTGATCTAGTGGAAGAAAGATCCAAATAAGATT 780
DB 935 GTTCTTATTTTTCGCTCTTCTTCTGATCTAGTGGAAGAAAGATCCAAATAAGATT 994
QY 781 TCTACATATGCAATGCTCTGCTGGGCGACAAATTAATGACAACTATTTGGTATGA 840
DB 995 TCTACATATGCAATGCTCTGCTGGGCGACAAATTAATGACAACTATTTGGTATGA 1054
QY 841 GACAAACCCCTTACCTTGGTGGGAAGATTGCTTTCGACAGGCTTTCCTCTGGC 900
DB 1055 GACAAACCCCTTACCTTGGTGGGAAGATTGCTTTCGACAGGCTTTCCTCTGGC 1114
QY 901 ATTTCTTCTTCTGCACTTCTGCGGATCTTGGCTCAGGTTTTCATTAAGTACAA 960
DB 1115 ATTTCTTCTTCTGCACTTCTGCGGATCTTGGCTCAGGTTTTCATTAAGTACAA 1174
QY 961 GACAAACCCCTTACCTTGGTGGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
DB 1175 GACAAACCCCTTACCTTGGTGGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1234
QY 1021 TGTGTTGGCGGATGAGTACAGCTGATGAGAAATGTTTCCATTTGCAACCTGGAAGCA 1080
DB 1235 TGTGTTGGCGGATGAGTACAGCTGATGAGAAATGTTTCCATTTGCAACCTGGAAGCA 1294
QY 1081 CACTTGAAGGCTTTCACACCTGACAGCCCTACCA----- 1115
DB 1295 CACTTGAAGGCTTTCACACCTGACAGCCCTACCA----- 1354
QY 1116 --TCGAAGCTTAAGTTTAAAGAGGAGTGGCATGCTTACCCCGAGGGGCAAGTATT 1173
DB 1355 AGTCGAAGCTTAAGTTTAAAGAGGAGTGGCATGCTTACCCCGAGGGGCAAGTATT 1414
QY 1174 AAGAGCGACAGGCTCAGTAGTGAGACAGAGGTCCCAAGACCGACATCAACGCGAG 1233
DB 1415 AAGAGCGACAGGCTCAGTAGTGAGACAGAGGTCCCAAGACCGACATCAACGCGAG 1474
QY 1234 GCGAGTCCCAACCAAGTGCAGAAAGTGCAGCTTCAACGACCGGCTTCCGCGCC 1293
DB 1475 GCGAGTCCCAACCAAGTGCAGAAAGTGCAGCTTCAACGACCGGCTTCCGCGCC 1534
QY 1294 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGTATGATGCTGACACAGCTTGGC 1353
DB 1535 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGTATGATGCTGACACAGCTTGGC 1594
QY 1354 ACTGATGATGATATGATGAAAGAAAGAGTCCAGTGTGATGATGATGATGATGATG 1413
DB 1595 ACTGATGATGATATGATGAAAGAAAGAGTCCAGTGTGATGATGATGATGATGATG 1654
QY 1414 CCACCACTTAAACCTGTCATTCAGCTATCAGAAATTATGAATTCATGTTGCAAAACGG 1473
DB 1655 CCACCACTTAAACCTGTCATTCAGCTATCAGAAATTATGAATTCATGTTGCAAAACGG 1714
QY 1474 AAGTTAAGGAAAGTTCAGTTCATATGATGATGATGATGATGATGATGATGATG 1533
DB 1715 AAGTTAAGGAAAGTTCAGTTCATATGATGATGATGATGATGATGATGATGATG 1774
QY 1534 GGTCACTGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1593
DB 1775 GGTCACTGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1834
QY 1594 GGAAGAGGGCAATTCATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAACATGAG 1653
DB 1835 GGAAGAGGGCAATTCATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAACATGAG 1894
QY 1654 ACCACAGAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713
DB 1895 ACCACAGAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1954
QY 1714 ATGAGTCCAGAGCTGAGTGCCTACTAGACATCTATCAACAGGTCCTCGGAAAGCTCT 1773
DB 1955 ATGAGTCCAGAGCTGAGTGCCTACTAGACATCTATCAACAGGTCCTCGGAAAGCTCT 2014

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QY 1774 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTGATGTGAACAGACATCT 1833
DB 2015 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTGATGTGAACAGACATCT 2074
QY 1834 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 1893
DB 2075 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 2134
QY 1894 TTATCCAGATCAACTAGTGGCAATCTCGAAGGCTGAGATTCATTCGAGCCAAAT 1953
DB 2135 TTATCCAGATCAACTAGTGGCAATCTCGAAGGCTGAGATTCATTCGAGCCAAAT 2194
QY 1954 GAGTTGAGTGGCCAGACTTTCTAGGCGCTTACGCTTACTAGTGAAGTCAAGCAACAG 2013
DB 2195 GAGTTGAGTGGCCAGACTTTCTAGGCGCTTACGCTTACTAGTGAAGTCAAGCAACAG 2254
QY 2014 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAAGCCCAACCAATTCGAAACCA 2073
DB 2255 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAAGCCCAACCAATTCGAAACCA 2314
QY 2074 ATTAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATCCCACTCTCTCCA 2133
DB 2315 ATTAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATCCCACTCTCTCCA 2374
QY 2134 GCCATCAGCATGTGCCAGGCGCAAGAACTCTGCAACCTTACGCTGAGGCTTACAGAA 2193
DB 2375 GCCATCAGCATGTGCCAGGCGCAAGAACTCTGCAACCTTACGCTGAGGCTTACAGAA 2434
QY 2194 AGCATTTCTGACGTCACACCTGCTTGTTCCTCCAGAGAAATGTTCAAGTTGACAG 2253
DB 2435 AGCATTTCTGACGTCACACCTGCTTGTTCCTCCAGAGAAATGTTCAAGTTGACAG 2494
QY 2254 TCAAATCTCAGCAAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2313
DB 2495 TCAAATCTCAGCAAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2554
QY 2314 TTGTCTGTCTGTCCCAATGGTGGGAGAACTTTGGGCAAAATCTTGTCTGTGCAAACTG 2373
DB 2555 TTGTCTGTCTGTCCCAATGGTGGGAGAACTTTGGGCAAAATCTTGTCTGTGCAAACTG 2614
QY 2374 ATCAGGTCGACCGAGAACTGAATATACACTTTCAGGAGAGTCAAGTGGCTCCAG 2433
DB 2615 ATCAGGTCGACCGAGAACTGAATATACACTTTCAGGAGAGTCAAGTGGCTCCAG 2674
QY 2434 GGCAGCCAAAGATTTTAAACCCAAATGAGGGAATCCAAATGTTTATTAATGTAAG 2493
DB 2675 GGCAGCCAAAGATTTTAAACCCAAATGAGGGAATCCAAATGTTTATTAATGTAAG 2734
QY 2494 GTGGGTCCGGAAGACAGACAGACACTTTGATGCGGCAAGGCTGCGCAAGGAA 2553
DB 2735 GTGGGTCCGGAAGACAGACAGACACTTTGATGCGGCAAGGCTGCGCAAGGAA 2794
QY 2554 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAAGATCATCTCAGACATTTGT 2613
DB 2795 GCTGCTTTGATCAGACTCTCTAAGAGTGAAGTCAAGATCATCTCAGACATTTGT 2854
QY 2614 AAGGCGAGAGAAATGACAGATGCGCTCAGCTTCCCTCATGTCAAACTGAATATA 2667
DB 2855 AAGGCGAGAGAAATGACAGATGCGCTCAGCTTCCCTCATGTCAAACTGAATATA 2908

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; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 19.1%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 3.6e-145;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1594 GGAAGAGGCAATCATCATGATAGAGAGCCGAGAGAAATACAGCAGACATGAG 1653
DB 1 GGAAGAGGCAATCATCATGATAGAGAGCCGAGAGAAATACAGCAGACATGAG 60
QY 1654 ACCACAGAGATCTCAGATGCTCGGTGGGTGTTCAAGTTGAAACAGGTACAGTCC 1713
DB 61 ACCACAGAGATCTCAGATGCTCGGTGGGTGTTCAAGTTGAAACAGGTACAGTCC 120
QY 1714 ATAGAGTCCAGTGGACCTGCTTACGATCTATGATCAACAGGTCTCTGGAAAGCTCT 1773
DB 121 ATAGAGTCCAGTGGACCTGCTTACGATCTATGATCAACAGGTCTCTGGAAAGCTCT 180
QY 1774 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTGAAATGTGAACAGACATCT 1833
DB 181 GCCTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTGAAATGTGAACAGACATCT 240
QY 1834 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 1893
DB 241 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGGCTGC 300
QY 1894 TTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTTCAATTCATTCGAGCCAAAT 1953
DB 301 TTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTTCAATTCATTCGAGCCAAAT 360
QY 1954 GAGTTGAGTGGCCAGACTTTCTAGGCGCTTACGCTTACTAGTCAAGTCAAGCAACAG 2013
DB 361 GAGTTGAGTGGCCAGACTTTCTAGGCGCTTACGCTTACTAGTCAAGTCAAGCAACAG 420
QY 2014 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAAGCCCAACCAATTCGAAACCA 2073
DB 421 GTGCCAATTAGTCAAGCCGATGGCTCAGAGTGGCAAGCCCAACCAATTCGAAACCA 480
QY 2074 ATTAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATC 2118
DB 481 ATTAATACGGACCCCAAGCCAGACGCCCAACCACTTTACAGATC 524

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RESULT 5
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guejler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A

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RESULT 6
US-09-949-016-1823
; Sequence 1823, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1823
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-1823

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Query Match	18.4%	Score 492;	DB 4;	Length 2196;
Best Local Similarity	59.3%;	Pred. No. 2.7e-139;		
Matches 1087;	Conservative	0;	Mismatches 555;	Indels 192;
				Gaps 7;

QY	217	TACGGCGGGGTGACAAATCTACTGTGACAAAGCGTCTGGAGAGACCCCGGGCGTGGCGTTTC	276
Db	181	TACCGCGCGCTGCAAACTGGGGGGTACAACTGCTGTGAGAGCGGCCCGCGCGTGGCGCTTC	240
QY	277	ATCTACCACGCTTTCGTTTTCTCCCTTGCTTTGGTGTCTGATTTTGTCAAGTGTTTCT	336
Db	241	GTTACCAACGCTTTCATATTTTGTGTGATCTTCAAGCTCGCTGTGTCTGTGTGTGTCC	300
QY	337	ACCATTCCTGAGCACAAAAATTGGCCTCAAGTTGCTCTTGATCTTGAAGTTCGTATG	396
Db	301	ACTATCCAGAGGACACAGAACTTGCCCAAGAGTGTCTTCATCTTGAATTCGTATATG	360
QY	397	ATTGTGCGCTTTGGTTTGGAGTTCATCATTTGGAATCTGTGTCGGGGTTCGTTGTGTGA	456
Db	361	ATCTGTGTTTTGCGCTTGGAGTACATCTTCGGGGTCTGTATCCGGATGCTGTCCGC	420
QY	457	TATAGAGGATGGCAAGAAAGACTGAGCTTTTGCTCGAAAGCCCTTGTGTTATATGATACC	516
Db	421	TACGAGGATGGCAGGGGTGCTTCGCTTTTGCAAAAGCCCTTGTGTATGACATTC	480
QY	517	ATTGTTCTTATGCTTCAATAGCAAGTGTTTCTGCAAAACTCAGGGTATATTTTTGCC	576
Db	481	ATCTGTGTGCGGCTCGGTGGCGGTCACTCCGCGGGGTACCCAGGGCAACATCTTCGCC	540
QY	577	ACGCTGTGACTCAGAAAGTCTCCGTTTCCATCAGATCCCTCCGATGTGTGCGATGGAACGA	636
Db	541	ACGTCCGCGCTGCGAGGATCGCTCTCTGCAAGTCTGCGATGTGTGCGATGGAACGCG	600
QY	637	AGGGAGGCACTTGGAAATTAAGTGGGTTCAAGTGTGTTATGTGCTCAGCAAGAAATTAATC	696
Db	601	CGGGCGGCACTGGAAGCTGCTGGGCTCAAGTGTCTAGCGGCAATGCAAGAAAGCTGATC	660
QY	697	ACAGCTTGGTACATPAGATTTTTGGTTCTTAATTTTTTGCTTTTCCTTGTCTATCTGGTG	756
Db	661	ACCCTGTGTACATCGGGTTCCTGGTGTCAATCTTCGCTCTCTTCTGTCTATCTGGCT	720
QY	757	GAAAGAGATGCCATTAAGAAGTTTTTCTACATATGAGATGCTCTCTGTGGGGGCACAATT	816
Db	721	GAGAAAGACGCCAATCCGACTCTCTCTCCATACGCCAGCATCGCTCTGTGGGGGCGAATT	780
QY	817	ACATTGCAACTATTTGGCTATGAGACAAAACTCCCTTAACCTTGGCTGGAGAAATTGCTT	876
Db	781	ACATTGCAACCAATCGGCTATGTGTACAGACACCGCAACATATGGCTGGGCAAGGTCCTG	840
QY	877	TCTGACAGGCTTTGCACTCTTTGGCAATTTCTTTCTTGTGCACTTCTGCGCGCAATCTTGGC	936
Db	841	GTGTGCTGGCTTCGCTTACTGCGGACATCTTTCTTTGTGCGTGTGCGCGGCAATCTTAAGC	900
QY	937	TCAGTTTTTGATTAAGTACAGAGACACACCGCCAGAAACACTTTGAAGAAAGAGG	996
Db	901	TCCGCTTTTGGCTCGAAGGTCCAGAGAGACACCGCCAGAAAGCACTTGAAGAGCGGAGG	960
QY	997	AACCCAGGTGCCAATCATTCAGTGTGTTTGGGCTATTTAGCAGCTGATGAGAAACT	1056
Db	961	ATGCTCGGAGCAACTTCATCCAGGCTGTCTGGCGCTGTACTCCACCGATATGAGCCGG	1020
QY	1057	GTTTTCATTGCAACTGGAAAGCAACACTTTGAAGGCTTGACAC-----	1100
Db	1021	GCTTACTGACAGCACCTGTGTACTATATGACAGTATCTTCCATCTTTCAGAGAGCTG	1080
QY	1101	-----	1100

Db	1081	GCCTCTTGTTAGACAGTGCAAAGGGGCCCGAAATGGGGGGCTTAAGGCCCTTGAGAGTG	1140
QY	1101	-----	1100
Db	1141	CGGCGGGCGCGGTATCCCGACGGAGACCTCCCGTTATCCCGCCGTTGGCACCCTGCGAC	1200
QY	1101	-----CTGCAGCCCTTACCAATCAGAAAGCTTAAGTTTAAAGAGCGA	1140
Db	1201	CGGCGGGGACAGCACTCTCTCTGCTGCGCTGGGGAAAGACCGGATGGGCAATCAAGACCGC	1260
QY	1141	GTGGCGCATGCTTACGCCCGAGGGGCTCAAGATTT-----AAGAGCGACAAAGCTTCAGTA	1194
Db	1261	ATCCGCATGGGCGACCTCCACGCGCGGACGGGTCCTTCCAAAGCAGCATCTGGCACCTTCCA	1320
QY	1195	GGTGACAGGAGTCCCCCAAGACCGGACATCAACAGCCGAGG---GCAGTCCCAACCAAGTG	1251
Db	1321	ACAATGGCCCACTCTCCCAAGCAGGAGCAGAGTGGGTGATGAGGCAACAGCCCAACCAAGTG	1380
QY	1252	CAGAAAGCTGGAGCTTCAAACGACCGAACCCTCTCGGCGCTTCGTCGCGCTTCAAAAGT	1311
Db	1381	CAAAAGAGCTGGAGCTTCAATGACCGGACCCGCTTCGGGCGATCTCGAAGCTC-----	1434
QY	1312	TCTCAGGCCAAAACCAAGTATGATGCTGACACAGCCCTTGGACCTGATGATGATATGAT	1371
Db	1435	-----AAACCCGCACTCTGCTGAGAGATGCC---CTTAGGAGAAATGACAGAG	1482
QY	1372	GAAGAAAGGATGCCAGTGTGATGATCATCGTGAAGACCTCAACCCCAACCACTTAAACCTGC	1431
Db	1483	GAGAAAGAGCTAACAGTGTGAGCTCAGCGTGGAGACATCATGCTGCTGTGTAAGACAGTC	1542
QY	1432	ATTGAGAGCTATCAGAAATTAAGAAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAACCTTA	1491
Db	1543	ATCCGCTTCATCAGAGATTTCTCAAGTCTCTGCTGGCCAAAAGAAATTCAGAGAGACACTG	1602
QY	1492	CGTCCATATGATGTAAGAAAGATGTCATTGGAACAATATCTCTGGTCACTGAGCATGTG	1551
Db	1603	CGACCGTATCAGACGTGAAGAGACGTCAATTGAGACAGTACACAGAGCCACCTGGAATCTG	1662
QY	1552	TGTAGAAATTAAGACCTTCAAACAGCTGTGATCAAAATCTTGAGAAAAGGCG---AAATC	1608
Db	1663	GCGCGGATCAAGAGCCTGCAAACTCGGCTGAGACCAAAATTTGGGTCGGGGGCCCGGGGAC	1722
QY	1609	ACATCAATTAAGAAAGAGCCGAGAGAAATTAACAGCACAACATGAGACCAAGACGATCTC	1668
Db	1723	AGGAAGGCCCGGGAGAAAGGGCGACAGAGGGGCCCTCCGACCGCGAGGTGGTGAATGAATC	1782
QY	1669	AGTATGCTCGGTCGGGTGATCAAGGTTGAAAAAACAGGTAACGTATCATTAGATCCAAAGCTG	1728
Db	1783	AGCATGATGGGAGCGCGGTGTCAAAGTGGAGAAAGAGGTGACGTTCATCGAGCAAAAGCTG	1842
QY	1729	GACTGCTTACTAGACATCTATCAACAGAGTCTTTGGAAGAGCTTGTGCTCAGCCCTGCT	1788
Db	1843	GACTGTGTTGGGCTTCTATTCGCGGTGCTCG-----GCTGTGGCACTCGGGCAGC	1896
QY	1789	TTGGCTTCATTCCAGATCCCAACCTTTTGAATGTGAACAGACATCTGACTTCAAGAGCCT	1848
Db	1897	CTGGGCGCCGCTGCAAGTGGCGGCTGTTGCACCCGACATCACTTCGACTACACAGGCTT	1956
QY	1849	GTCGATAGCAAAAGATCTTTTCGGGTTCCGCAAAA	1882
Db	1957	GTCGACCAACGAGCAGATCTCCGTCTCCGACACAGA	1990
RESULT 7			
US-09-492-361-1			
; Sequence 1, Application US/09492361			
; Patent No. 6794161			
; GENERAL INFORMATION:			
; APPLICANT: JENTSCH, Thomas J.			
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE			
; TITLE OF INVENTION: POTASSIUM CHANNELS			
; FILE REFERENCE: 2815-127P			
; CURRENT APPLICATION NUMBER: US/09/492.361			

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1 CURRENT FILING DATE: 2000-01-27
2
3 NUMBER OF SEQ ID NOS: 41
4
5 SOFTWARE: PatentIn Ver. 2.1
6
7 SEQ ID NO 1
8
9 LENGTH: 2335
10
11 TYPE: DNA
12
13 ORGANISM: Homo sapiens
14
15 FEATURE:
16
17 NAME/KEY: gene
18
19 LOCATION: (1)..(2335)
20
21 NAME/KEY: CDS
22
23 LOCATION: (83)..(2170)
24
25 OS-09-492-361-1

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Query Match	18.4%;	Score 492;	DB 4;	Length 2335;
Best Local Similarity	59.3%;	Pred. No. 2.9e-139;		
Matches 1087;	Conservative	0;	Mismatches 555;	Indels 192;
				Gaps 77;

Qy	217	TACGGCGGGGAGACAACTACCTGTACAAACGCTGTGAAGAACCCCGCGGCTGTGGCGTTTC	276
Db	320	TACCGCGCGCTGTGACAACTGGGTCTACAAACGTGTGTGAGCGGCCCCCGCGGTGGGACTTTC	379
Qy	277	ATGTACCAACGCTTTCGTTTTCTCCCTGTCTTGGTGTCTGTGATTTTGTACAGTGTTTTCT	336
Db	380	GTTACCAACGCTTTCATATTTTGTGTGGTCTTCACTGCTGTGTGTCTGTCTGTGTGTCTTC	439
Qy	337	ACCATCCCTGAGACACAAAATTTGGCTTCMACTTGCCTTGTATCTTGATCTGTGAATTCGTATG	396
Db	440	ACTATCCAGAGACACAGAACTTGGCCCAACGAGTCTCTCATTTTGGAAATTCGTATG	499
Qy	397	ATTGTGCTTTGGTTTGGAGTTCATTCATTCGATCTGTGCGGGTGTGCTGTGTGTGCA	456
Db	500	ATGTGTGTTTTCGCTTGTGAGTACATCTGCGGGTCTGTGTCCGCGGATGTCTGTGTGCGCC	559
Qy	457	TATAGAGATGTGACAGAAAGACTGAGTTTGTCTGAAAACCTCTTGTGTATATAGATACC	516
Db	560	TACGAGAGATGTGACAGGATCGCTTCGCTTGTGCAAAAACCTTCTGTGTATCATCACTTTC	619
Qy	517	ATTGTCTTATCGCTTCATATAGACATTTTGTCTGTGAAAACCTCAAGGTATATTTTTC	576
Db	620	ATGTGTGTGTGGCTTCGGTGGCCGTCAATCGCGGGGTATCCCAAGGCAATCTTTCGCC	679
Qy	577	ACGTCTGCATCAGAAAGTCTCCGTTTTCTTACAGATCTCCGATGTGTGCGATGTGACGGA	636
Db	680	ACGTTCGGGCTGTGCGAGATGGCTTCTGTGAGATCTGTGCGATGTGTGTGTGTGTGTGACCGC	739
Qy	637	AGGGAGGCACTTGGAAATTACTGGGTTCAGTGTATATGCTCACAGCAAGAAATTAATC	696
Db	740	CGCGCGGCACTGTGAACTGTGGGCTCAGTGTCTTACGCGCATATGACAAAGAGCTGTATC	799
Qy	697	ACAGCTTGATACATAGAAATTTTGGTTCATATTTTGTGCTTTCCTGTCTCATCTGTATG	756
Db	800	ACCCCTGTGTACATCGGATCTCGTGTGTCTCATCTTGCCTCTTCTGTGTCTTCACTGTGCC	859
Qy	757	GAAGAAGTGCATAAAGAGTTTTCTTACATATAGAGATGTCTTGTGTGGGACAAAT	816
Db	860	GAGAAAGACGCAACTCCGACTTCTCTCTTACGCGCATCGCTCTGTGTGGGAGACAT	919
Qy	817	ACATTTGACACTATTTGGCTATAGAGACAAAACCTCCCTTAATCTTGGCTGTGAAATTTGCT	876
Db	920	ACATTTGACAACTATGCTATGTGTGACAAACACCGCACACATGTGCTGTGGCGGGTCTCTG	979
Qy	877	TCTGAGGCTTGTGACCTCTTGGGACTTCTTCTTGTGACATTCGACGGGACTTGTGGC	936
Db	980	GCTGTGTGCTTGTGCTTACTGTGGACATCTTCTTGTGCTGTGCTGTGCGGCAATCTTAGGC	1033
Qy	937	TCAGTTTTGCATTTAAAAGTACAGAAACAACCGCACGAAACAATTTGAGAAAAAGAG	996
Db	1040	TCCGGCTTTGGCCCTGAAGTCCAGAGACGACCGGCAAGAGCACTTGAGAAAGCGAGG	1099
Qy	997	AACCCAGCTGCCAACTCATTTCAGTGTGTGTGGGTAGTTACGACAGCTGTATGAGAAATCT	1056
Db	1100	ATGCGCGAGGCAACCTTATCCAGGCTGTGTGCGGCTGTATCTCACCGATATATGTGCGG	1159

Qy	1057	GTTCCTCAATTGGAACCTTGAAAGCCACACTGTAAAGCCCTTGGACAC-----	1100
Dp	1160	GCCCTACCTGAAAGCCACCTGTGTACTACTATGACAGTATCTCTCCATCTTTCAGAGACTG	1219
Qy	1101	-----	1100
Dp	1220	GCCTCTTTGTTTGTAGCAGTGTACAGGGGCCGGAATG9999CCTAACG99CCCTTG9AGGTG	1279
Qy	1101	-----	1100
Dp	1280	CGGCGGGCGCCGGTATCCCGACGAGACACCTTCCCGTTAACCGCCGTTGCCACTGCGAC	1339
Qy	1101	-----CTGCAGCCCTTACCAATCAGAAAGCTAAAGTTTAAAGAGCGA	1140
Dp	1340	CGGCCGGGACGACACCTCTCTTCTGCTCGTGGGAAAGACCGGGATGGGACTCAAGACCGC	1399
Qy	1141	GTGCGCATGTGCTAGCCCCCAAGGGCCAGAGTAT-----AAGACCGACAAAGCCTCAGTA	1194
Dp	1400	ATTCGGCATGGGACAGCTCCACAGCGCGGACGGGTCTTTCAAAGCAGCAGCTGGACCTTCCA	1459
Qy	1195	GGTACACAGAGTCTCCCAAGCACCCGACATCACAGCCGAG--GCAGTCCCAACAAAGTG	1251
Dp	1460	ACAATGCCACCTTCCCAAGCAGGACAGAGTGGGTAGAGGCAACACGCCCCACCAAGGTG	1519
Qy	1252	CAGAAAGACTGAGACTTCAACGACCGAACCCTTCGCGCCCTCGCTGCGCCTCAAAAGT	1311
Dp	1520	CAAAAGAGCTGTGAGCTTCAATGACCGCACCCGCTTCCGGGAGATCTCTGAGACTC-----	1573
Qy	1312	TCTCAGCCAAACCGATGATAGATGTCTGACACAGCCCTTGGACCTGATGTATATGAT	1371
Dp	1574	-----AAACCCCGCACCTCTGCTGAGGAGTCCC-----CTTCAGAGAAAGTGTAGCAGAG	1621
Qy	1372	GAAGAAGATGCCAGTGTGATGTATCTAGTGGAAACCTCACCCACCACTTAAACGTGC	1431
Dp	1622	GAGAAAGACTACAGCTGTGTAGCTCAGCGTGGACACATCATGCTGTGTGTAAACAGCTC	1681
Qy	1432	ATTTCGAGCTATCAGAAATTATGAATTTTCATGTTGCCAAAACGGAAGTTTAAAGAAACGTTA	1491
Dp	1682	ATTCGGCTCAATCAGAGATTTCTCAAGTTCTGTGTGCCAAAAGGAATTCAGAGACACTG	1741
Qy	1492	CGTCCATATGATGTAAAGATGTCTATTGAAACATATTTCTGTGTGTCATCTGTGACATGTTG	1551
Dp	1742	CGACCGTACGACGTGAAGGACGTCTATTGAGAGTACAGAGGCCACCTGTGACATGTGTG	1801
Qy	1552	TGTGAATTTAAAGCCCTTCAAAACAGTGTTGATCAAAATTTCTGTGAAAAGGCG--AAATC	1608
Dp	1802	GCGCGGATCAGAGACCTGTGCAAACTCGGGGTGTGACCAAAATTTGTGGGTCCGG999CCCGGGAC	1861
Qy	1609	ACATCAGATTAAGAAAGACCCGAGAGAAAATTAACAGCAGAACATGTAGACCAAGACGATCTC	1668
Dp	1862	AGGAAGGCCCGGGAGAAAGGGGGACAAAGGGGCCCTCCGACGGGAGGTGTGTGATGAATC	1921
Qy	1669	AGTATGCTCGGTGGGTGTCTCAAGTTGAAAACAGGTACAGTCTCATAGAGTCCAAAGTGT	1728
Dp	1922	AGCATGTATGGGACCGGTGTGTCAAGTGTGAAGAAAGAGTGTGACGTCTATCGACCAAACTGTG	1981
Qy	1729	GACTGACCTACAGACATCTATCAACAGAGTCTCTTGGAAAAGGCTGTGCCTCAGCCCTGCT	1788
Dp	1982	GACCTGCTGTGGGCTCTATTTGCGCGTCTGC-----GCTTGGCACCTCGGCGACG	2035
Qy	1789	TTGGCTTCATTTCCAGATCCACCTTTTGAATGTGAAACAGACATGTGACTATCAAGCCCT	1848
Dp	2036	CTGGGACCCGTGCAAGTGTGCGCTGTTGCAACCCGACATCACTTCGACTACCAAGCCCT	2095
Qy	1849	GTCGATAGCAAAAGTCTTTGGGTTTCGGCACAA	1882
Dp	2096	GTGGACCAAGAGCATCTCCGTCTCTGCGACAGA	2129

RESULT 8
US-09-177-650-88
; Sequence 88, Application US/09177650

Patent No. 643719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCES: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/065,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 88
LENGTH: 2273
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(12271)
US-09-177-650-88

Query Match 18.3%; Score 489.2; DB 3; Length 2273;

Best Local Similarity 57.0%; Pred. No. 2e-138; Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;

QY 64 GGCTCTGCTAGTGTGGGCAACCGCGCGGCGAGCTTGTGTGGGCGCGGTGGCTTGAAG 123
DB 67 GGGCTGTGGGGGTGAGACCCCGCGCGCGCGAGTCCAGACGCGAGCGCGCNCCTACTCATC 126
QY 124 GAGAGCGCGCGGGGCAAGAGAGGGGCGCGGATGAGCTCTGGGAAAGCGCTCTTTAC 183
DB 127 GCGGGCTCCGAGGCGCCCAAGCGCGCGCANCNTTTGAGCAAGCGCGGAGCGGCGCG 186
QY 184 AGCAGTACGCAAGCTCGCGCGCGCAACCTTCAGTACCGGCGGTGAGAACTACCTGTAC 243
DB 187 GGANCCGGGAAGCGCCCNANCGCAAGCGCTTCTACCGCAAGCTGCAAAATTTCTCTAC 246
QY 244 AACGTCCTGAGAGAGACCCCGCGCGCTGGGCGTTCATCTACAGCTTTCGTTTTCTCTT 303
DB 247 AACGTCCTGAGAGAGACCCCGCGCGCTGGGCGTTCATCTACAGCTTTCGTTTTCTCTT 306
QY 304 GTCCTTGTGCTTGAATTTGTACGTGTTTTCTACCATCTCGAGACACAAATTTGCGC 363
DB 307 GTTCTCTCCGCTTGTGCTTCTGTGTTTTCCACATCAAGAGTACGAAAGAGCTCT 366
QY 364 TCAGATGCTCTGATCTCTGAGTTCGATGATGATGATGATGATGATGATGATGATG 423
DB 367 GAGGGGCGCTCTACATCTTGAAATCGTACTATGCTGATGCTGCTGCTGCTGCTGCTG 426
QY 424 ATTGATCTGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
DB 427 GTGAGATCTGCGGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
QY 484 TTGCTCGAAAGCGCTTCTGTGTATGATGATGATGATGATGATGATGATGATGATG 543
DB 487 TTGCTCGAAAGCGCTTCTGTGTATGATGATGATGATGATGATGATGATGATGATG 546
QY 544 GTTTCGCAAAAACCTAGGATATATTTTGCACCTGCACTGCACTGCACTGCACTGCT 603
DB 547 CTGGCTGCTGCTTCCAGGCAATGCTTTTGCACATGCTGCTGCTGCTGCTGCTGCTG 606
QY 604 CTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
DB 607 TTGCAAAATCTTGGGATGATCCGTATGAGACCGAGGGGATGAGACCTGGAAGCTCTT 666
QY 664 TGAAGCTTTATGCTCAAGCAAGAAATTAATCAAGCTTTGATGATGATGATGATGATG 723
DB 667 TCGGTAGTCTAGCTCAAGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
QY 724 CTATATTTTTCGCTTCTCTGCTATCTGCTGCAAAAGATGCCAATAAAGATTTTCT 783

DB 727 CTCATCTCGGCTCATTTCTGTGTATCTGGGAGAAAAGGAGAAATGACCATTTGAC 786
QY 784 ACATATGAGATGCTCTCGGAGGGGCAAAATTAATTAATTAATTAATTAATTAATTAAT 843
DB 787 ACTATGAGATGCTCTCGGAGGGGCTGATCACCCTGACCAATTAATTAATTAATTAAT 846
QY 844 AAAACTCCCTAACTTGGCTGGAAAGATTTCTTGTGAGGCTTGTGACTCTCTGCAAT 903
DB 847 AAGTACCTCAGACCTGGAGCGGAGGCTGCTGCGAGCACTTACCTCATTTGATGCTG 906
QY 904 TCTTTCTTTGACTTCTCGCGGCAATTTCTGCTCAGGTTTGTGCAATTAATTAATTA 963
DB 907 TCGTTCTTTGCTCTTCCGCTGCGATTTTGGATCCGCTTTGCTGAAATTCGAAGG 966
QY 964 CAACCGCGCAAGAAACCTTGTGAGAAAGAAAGAACCCAGCTGCCAATCTTCAAGT 1023
DB 967 CAGCATCGGCAAAAACCTTTGAGAAACGGCGAACCCTGCGGCAAGTCTGATCCAGT 1026
QY 1024 GTTGGCTGATTAAGCACTGAT----- 1047
DB 1027 GCTGAGATTTCTATGCTACTTAACCTTCACGACCGACTGCTCAGCGTGGAGTAC 1086
QY 1048 ---GAGAAATCTGTTCCATTTGCAACCTGGAAGCCACCTTGAAGCCCTTGCACCTGC 1104
DB 1087 TACGAGCGNACAGTCACTGCTCCCATGTACAGCTTCAAACTCAAACTTAAGGGCTCTC 1146
QY 1105 AGCCCTTACC-----AATCAGAACTTAAGTTTAA 1132
DB 1147 AGATCATCTCCACCTTGAACCAAGTGAAGCTGCTGAGAGAAATCTCAAGAGAAATCTG 1206
QY 1133 AGGACGAGTGGCGATGCTGAGCCCGAGGGGCAAGATTAAGAGCGGACCAAGCTTCA 1192
DB 1207 CTACCTTCAAGAAAGAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1266
QY 1293 TAGGTGACAGGAGTCCCAAGCAACCGACATCAAGC----- 1229
DB 1267 AAGGAGAAAGGGGTCTCCAGAGCCAGAGGCTCGGCGGCTCCCAAGTCCGATCAGAT 1326
QY 1230 --CGAGGCGAGTCCCAAGCAAGAGTGAAGCTTCAAGCAAGCCGCTTTC 1287
DB 1327 CTGATGACAGCGCGAGAGAGGTGCGCAAGAGCTTGAAGCTTGTGAGCGGCGGACA 1386
QY 1288 CGGCTCTGCTGCGCTTAAAGTTCTCAGCCAAAACAGATGATGATGCTGACACAGCC 1347
DB 1387 CGCCAGGCTTCCGATCAAGGCTGCTCATCCCGCGAAATTCGAAAGAAAGCAAGCCCTC 1446
QY 1348 CTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1407
DB 1447 CTTGGAGAGACATGTGAGAGCAACAGAGCTTAACTGCGATTTGTGACTGAGAT 1506
QY 1408 CTACCCCAACCACTTAAATCTGATTCAGCTATCAGATTAATTAATTAATTAATTAAT 1467
DB 1507 CTTACCTCTGGGCTCAAAATTAAGATCAGAGCGGTGTGTATGCTGCTGCTGCTGCT 1566
QY 1468 AAACGAACTTAAAGAAAGCTTACGCTCATATGATGATGATGATGATGATGATGAT 1527
DB 1567 AAGCAAAAGTTCAAGAGAGTCTGCGCCATATGATGATGATGATGATGATGATGATG 1626
QY 1528 TCTGCTGATCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1587
DB 1627 TCGGCTGAGCACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1686
QY 1588 ATTCTTGAAGAAAGGCAATCAATCAGATTAAGAGCCGAGAGAAATTAACAGCAG 1647
DB 1687 ATTGTGGGGCGGGGCGCAAAATTAAGATTAAGGATTAAGGATTAAGGATTAAGG 1743
QY 1648 CATGAGACCAAGAGATCTGATGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1707
DB 1744 ACGAGCTGCCCGAGAGCCCAAGATGATGAGAGCTTGGAGAGAGTGAAGAAAGAGT 1803
QY 1708 CAGTCCATAGAGTCCAGCTGAGCTGCTTACATGAGCATCTTACAG 1755

Db	121	ATGAAATCCAAAGCTGGACTGCTTACTAACAATCTATCAACAGGTCCTTTCGGAAAGGCTCT	180
Oy	1774	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1833
Db	181	GCCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	240
Oy	1834	GACTATCAAAAGCCCTGTGGATATGCAAAAGATCTTTTGGGTTCCGCACAAAACAGTGGCTGC	1893
Db	241	GACTATCAAAAGCCCTGTGGATATGCAAAAGATCTTTTGGGTTCCGCACAAAACAGTGGCTGC	300
Oy	1894	TTATCAGATCAACTAGTGGCCAAACCTCGAAGGSCCTGCAGTTTCATTCGACGCCAAT	1953
Db	301	TTATCAGATCAACTAGTGGCCAAACCTCGAAGGSCCTGCAGTTTCATTCGACGCCAAT	359
Oy	1954	GAGTTCAGTGGCCAGACATTTCTACGCGCTTAGCCCTTACTATGACACAGTCAAGCAACAG	2013
Db	360	GAGTTCAGTGGCCAGACATTTCTACGCGCTTAGCCCTTACTATGACACAGTCAAGCAACAG	417
Oy	2014	GTGCCAATTTAGTCAAAAGCATGGCTCAGACAGTGGCAGGCACACCAACCATTTGCAACCGAA	2073
Db	418	GTGCCAA-TAGTCAAAAGCATGGCTCAGACAGTGGCAGGCACACCAACCATTTGC-AACTAA	475
Oy	2074	ATTAATTAAGGCAACCCAAAGCCAGACAGCCCCCAACAATTTCACAGATCCCACTCTCTT	2129
Db	476	ATTAATTAAGGNAACCCAAAGCCAGACAGCCCCCAACAANTTTCAGTCTCTCTTCAGCTCT	531

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RESULT 12
US-09-105-058C-26
/ Sequence 26, Application US/09105058C
/ Patent No. 6403360
/ GENERAL INFORMATION:
/ APPLICANT: Blamar, Michael A.
/ APPLICANT: Dworetzky, Steven
/ APPLICANT: Gribkoff, Valentin K.
/ APPLICANT: Levesque, Paul C.
/ APPLICANT: Little, Wayne A.
/ APPLICANT: Neubauer, Michael G.
/ APPLICANT: Yang, Wen-Pin
/ TITLE OF INVENTION: KNO2 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
/ FILE REFERENCE: 3053-4052
/ CURRENT APPLICATION NUMBER: US/09/105,058C
/ CURRENT FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 60/055,599
/ PRIOR FILING DATE: 1997-08-12
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 2565
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-105-058C-26

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Query Match	16.0%;	Score 427.2;	DB 3;	Length 2565;
Best Local Similarity	56.7%;	Pred. No. 2,1e-119;		
Matches 923;	Conservative 0;	Mismatches 648;	Indels 57;	Gaps 5;

Qy	13	GAAGTGGGCGCGGAGGAGTGTCTGTAACTTCGACAGCCGCCAGGGGCGAGCGGCTTGTA	72
Db	43	GCGGGGGGCGCGCGGAGCGAGGAGGGGAAAGTGGGGAGCTGGCGCCCGGCGGAGCGTGGAGCAA	102
Qy	73	CTGCTGGGCACTCCGCGCGGCCACGCTTGTGGTGGCGGCGGGTGGCTTGAAGGAGAGCGCG	132
Db	103	GTCACCTTGGCGCTTGGGGGCGCGAGCCGACAAAGACGGGAGCCCTGTCTGTGGAGGGGCGGC	162
Qy	133	CGGGGCAAGCAGAGGGGCGCGAGTGAAGCTGTGGGGAAGCGCGTCTTTCACAGAGTAGC	192
Db	163	GCGCGCGAGAGGGGCGAGGAGACCCCGCAGGGGCAATGGGCTCTTGCCAAAGACCCCG	222
Qy	193	CAGAGCTGCC-----GGCGCAAGCTGAAGTACCGCGGGGTGCAGAACTACTGTGAC	243
Db	223	CTGAGCCCCCGAGTCMAAGAGAAACAAGCCCAAGTACCGGCGGATCCAACCTTGTGATCAC	282

QY	244	AACGTGCTGAGAGAACCCCGCGCTGGCGTTCACTACACGCTTTCGTTTTCTCTCT	303
Db	283	GACGCCCTGAGAGAACCGCGGGCGCTGGCGCTGCTTTTAAACAACGGTGGTTCCTATT	342
QY	304	GCTTTGGTGGCTGATTTTGTCAAGTGTTTCTACATCCCTGAGGCAACAATAATGGCC	363
Db	343	GTCCGGGGTCTTGATTTCTGGCTGTCCGACCACTTCAAGAGATAGAGCTGTCTCG	402
QY	364	TCAAGTTGGCTCTTGATCTGGAATGCTGATATGATATGCTCTTGGTTTGGATTCATC	423
Db	403	GGAAGCTGCTCTTGTTACTGGAACATTTGCTATTTTCACTTTTGGAGCCGATTTGCT	462
QY	424	ATTGGAATCTGCTCTGCGGGTTCGTGTTGTCGATATAGAGATGGCAAGAGACTAGG	483
Db	463	TTGAGGATCTGGGCTGCTGATGTGTTGCTCGGATACAAAGGCTGGCGGGCCGACTAAG	522
QY	484	TTTGTGCGAAGCCCTTCTGTGTATAGATACATTTGTTCTTATTCGCTTCAATAGCATT	543
Db	523	TTTGCAGAGAAAGCCCTGTGTGATTTGGACATCTTTGTGCTGATTTGCTCTGTGCGCAGTG	582
QY	544	GTTTCTGCAAAAACCTCAGGGTAATATTTTTGGCCAGTCTGCACTCAAGCTCCGTTTC	603
Db	583	GTGTGCTGGGAAAACCAAGGCAATGTTCTGTGCGCACT---CCCTGCGAAGCTGCGCTTC	639
QY	604	CTACAGATCTCTCGCATGTGCGCATGAGCCGAAGGGGAGGCACTTGGAATTACTGAGT	663
Db	640	CTGCAGATCTCGGCATGCTCGGATGGAACGGAGAGAGTGGAACCTGGAAGCTTCTGGCG	699
QY	664	TCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTCATAGATTTTTCGTT	723
Db	700	TCAGCCATCTGTGCGCCACAGCAAGAACTCATCGGCTGTGTACATCGGTTTCTGACA	759
QY	724	CTTATTTTTCGTCTTCTTCTGTCATCTGGTGGAAAAGATGCG-----768	
Db	760	CTCATCTCTTCTTCAATTTCTGTCTACTGCTGTAGAAAGACGTCCAGAGGTGAGATGCA	819
QY	769	-----AATPAAGATTTTCTACATATGCAATGCTCTCTGGTGGGACACA	813
Db	820	CAAGGAGAGAGATGAAGAAGAGATTTGAGACTATGCAAGATGCTGTTGGTGGGCTG	879
QY	814	ATTACATTGACAACTATTGGCTATAGGAGACAAACTCCCTTACTTTGGCTGGAGAGATTG	873
Db	880	ATCACACTGGCAACATTTGGCTATAGGAGACAAACCAACCAAAAGTGGGAAGGCGCTG	939
QY	874	CTTTCTGAGGCTTTGCACTCCTTGGGCAATTTCTTTTGGCACTTCGCGCGGCACTTCTT	933
Db	940	ATTGCGCGACCTTTTCTTAAATTTGGGCTCTCTTTTTCCTTTCGACGGGATCTTG	999
QY	934	GGCTCAGGTTTGGATTTAAAGTACAAAGAACACACCGCCAGAAACCTTTGAGAAAAGA	993
Db	1000	GGGTTCGGGCTGGCGCTCMAAGTGTCAAGAGAACACCGTCAAGAGCACTTTGAGAAAAGG	1059
QY	994	AGGAACCCAGCTGCCAATCTCATTTCAGTGTGTTTGGCGTAGTTACGCACTGATGAGAA	1053
Db	1060	AGGAAGCCAGCTGCTGAGCTCATTTCAAGGCTGCTGAGAGTATTTGTACCAACCCCAAC	1119
QY	1054	TCTGTTTTCATTG-----CAACTGGAAGCCACACTTGAAGGCTTGGCAACCTGC	1104
Db	1120	AGGATTAAGCTGTGGCGGACATGGAGATTTTATGAATACAGTCCTTTTTCCTTTCTTC	1179
QY	1105	AGCCTTACCAATCAGAAAGCTAAGTTTAAAGGAGGAGTGGCATGAGTCCCAAGGGGCG	1164
Db	1180	AGGAAGAAGACGTCTGGAGGACGATCCAGCCAAAGCTGGGTCTCTTGGATCGGGTTGCG	1239
QY	1165	CAGAGTATTAAGACCGACAAAGCTCTCAGTAGGTGACAGAGGTGCCCAAGCACCGACATC	1224
Db	1240	CTTTCTAATCTCGTGTAGCAATACTTAAAGAAAGCTATTTTACCCTCTGAAATGTAGAT	1299
QY	1225	ACAGCCGAGGCAATCCCAACCAAGTGCAGAAAGCTGGAGCTTTCACAGACCAACCGCG	1284
Db	1300	GCCATTAAGAAAGATCTTTCTTAAAGAACAAAGCTGTGGCTTTAAACAATTAAGAGCT	1359
QY	1285	TTCCGGCCCTGCTGCGCCTCAAAAAGTTTTCAGCCAAAACAGATGATAGATGCTGACACA	1344

DB	1300	GCCATAGAAAGAAAGTCCCTCTAAGAAGAACCAAGCCTGTGGCTTAAACCAATAAAGACGCT	1359
OY	1285	TTCCGGCCCTGCCTGCGCTCAAAAGTTCTCAGCCAAAACGAGTATAGATGCTGACACA	1344


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Db      1072 GGGTCGGGGGTCGGCCCTCAAGTGCAGAGACCAACCGCTGACGAAGACCTTTGAGAAAAG 1131
Qy      994 AGGAAGCCAGCTGCAACCTCATTCACTGCTGTTGGCTAGTATACGACGTATGAGAAA 1053
Db      1132 AGGAAGCCAGCTGCTGATCTTCAAGCTGCTGAGGATATATGATACCAACCCCAAC 1191
Qy      1054 TCGTTTCAATG-----CAACCTGGAAGCACAATTGAAAGGCTTGACACCTGC 1104
Db      1192 AGGATTACCTGGTGGGACATGAGATTTTATATCACTGCTCTTTTCTTTCTTC 1251
Qy      1105 AGCCCTACCAATCAGAACTAAGTTTAAAGAGCGAGTGGCATGAGCTTACCCGAGGAGC 1164
Db      1252 AGGAAGAACAGCTGAGGAGCATCCAGCAAAAGCTGGGTCTCTTGATCGGGTTCCG 1311
Qy      1165 CAGAGTTTAAAGCCGACAAAGCTCAGTAGTGCACAGAGTCCCAAGACCGACATC 1224
Db      1312 CTCTTAAATCCTGCTGATGCAATATCTAAAGAAAGCTATTTACCCCTGGAATGTAGAT 1371
Qy      1225 ACAGCCGAGGCACTGCCACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGC 1284
Db      1372 GCCATGAGAAAGTCTCTTAAAGAACAAAGCTGCTGCTTAAACAAATTAAGAGCGT 1431
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Qy      1345 GCCCTTGGCACTGATGATGATATGATGAAAGAGATGCCAGTGTATGATCAGTGA 1404
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Qy      1405 GACCTCACCCACCACTTAAAGCTGATTCGAGCTATCAGAAATTATGAATTTCAATGTT 1464
Db      1546 GACATGATCCCACTGAGAGGCGCCATCGAGCCCTCAGAAATTTCAAAATTCCTGCTC 1605
Qy      1465 GCAAAACGAAAGTTTAAAGAAAGCTTACGTCAATGATGTAAGAAAGTCAATGAAACA 1524
Db      1606 TATTAATAAAATTTCAAGAGACCTTTGAGGCTTAAAGATGAAAGATGATGAGCAG 1665
Qy      1525 TATTCGCTGCTCATCTGACATGTTGTGATGAAATTAAGCCTTCAACACGTTGAT 1584
Db      1666 TATTCGCTGCTGCTGATCTGACATGCTTTCAGAGTAAAGTACCTTCAGACGAATGAT 1725
Qy      1585 CAATTCCT 1592
Db      1726 ATGATTTT 1733

RESULT 14
US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)

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US-09-177-650-90
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Best Similarity 56.9%; Pred. No. 36-113;
Matches 926; Conservative 3; Mismatches 640; Indels 57; Gaps 6;

Qy      15 GTCGGGCGGGGAGGAGTGTCTGTAACCTCGGACGCGCCAGGGGCGACGCGCTGTACT 74
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Qy      75 GCTGGACCCCGCGCGCAACGCTTGTGGCGGCGGTGGCTGAGGAGAGCGCGCG 134
Db      354 CACCTTGGCGCTAGGGCGCGAGCCGACAAAGACGGGACCTGCTGTGAGGCGGTGG 413
Qy      135 GGGCAAGCAGGGGCGCGGATGACCTGCTGGGGAAGCCGCTCTTTACACAGATGCCA 194
Db      414 CCGGAAAGAGGGGAGAGAGACCCCGAGGGGCACTGGGCTCTTGGCAAAAGCCCCCT 473
Qy      195 GAGCTGCC-----GGCGCAAGCTCAAGTACCGCGGGGTGCAGAACTACCTGTACAA 245
Db      474 GAGCCGCCAGTCAAGAGAACACCCCAAGTACAGGCGCATCCAACTTTGATCTATGA 513
Qy      246 CGTGTGAGAGACCCCGCGGCTGGGCGTTCACTCAACGCTTTGTTTTCTCTTGT 305
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Db      774 TGCAGAAAGCCCTGTGATGATGATGATCTTGTGATGATGCTCTGTGCAATGAT 833
Qy      546 TTTCGAAAAATCAGAGTAATATTTTTCACAGTGTGACATCAGAGTCTCCGTTTCT 605
Db      834 TGCCTGGGAAACAGAGGCAATCTTTGGCCACT---CCCTCGAAGCTTCTGCTTCT 890
Qy      606 ACAGATCTTCGCGATGTCGATGAGACCGAAGGGAGGCACTTGGAAATTAATCTGAGTTC 665
Db      891 GCAGATCTCGCGATGCTTCAATGATAGAGAGGGGTGGCACTTGGAACTCTTGGGCTTC 950
Qy      666 AGTGTATATGCTCAAGCAAGAAATTAATCAAGTGTGTATATGATTTTGGTTCT 725
Db      951 GGTATCTGTGCGCCAGAGAAAGAACTCACTATGCTGTGTATATGAGGCTTCTGACACT 1010
Qy      726 TATTTTGTCTCTTCTGTCTATCTGTGTAAGAAAGAT-----766
Db      1011 CATCTTTTCTTATTTCTTGTCTTCTGATGTAAGAAAGATGTCAGAAATGATGCCA 1070
Qy      767 -----CCAAATAAGATTTTCTAATATGAGATGCTCTGTGTGGGCAAT 815
Db      1071 AGGAGAGAGATGAAGAGAGATTTAGACCTATGAGATGCTCTGTGTGGGCTGAT 1130
Qy      816 TACATTGACAATATGCTATGAGACAAAACTCCCTTAATCTGTGCTGGAAAGATTTGCT 875
Db      1131 CACACTGGCACCATTTGTTATGAGACACCACTAAACCTGGGAAGAGCTGTGAT 1190
Qy      876 TTTCGAGGCTTTCGACTCTTGGCAATTTCTTTCTTTGACTTTCGCGGCAATTTCTTG 935
Db      1191 TGTGCGACCTTTTCTTATGAGGCTCTCTTTTGTGCTTCCGCGAGGATCTTGTG 1250
Qy      936 CTCAGGTTTTCATTAAGATCAAGAACACCGCCAGAAACCTTTGAGAAAGAG 995
Db      1251 CTCAGGATGCTGATGAAGTTTCAAGAGACAGCGTCAGAAAGCACTTTGAGAAAGAG 1310

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Qy	996	GAACCGACGTCGCAACCTCATTCAGTGTGTTGGGTAGTAAACGACGTG---TGAAA	1052
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Qy	1053	ATCTGTTTCATTGGCAACTGGA-----AGCCACACTTGAAGGCTTGCACACCTGCAG	1106
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Qy	1107	CCCTAACCAATCAGAAAGCTAAGTTTAAAGACGAGTGGCATGGCTAGCCCCAGAGGCCA	1166
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Qy	1167	GAGTATTTAAGACCGCAACAGCCTCAGTGTGACAGAGGTGCCCAAGACACCAATCAC	1226
Db	1491	TTCTATCTCTGTGGTAGCAATCTAAAGAAAGTATTACCCCTCGAATGTAGATGC	1550
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Qy	1347	CCTTGGCACTGATGATATATATGATGAAGAAAGATGCCAGTGTATATCATGTGAGAGA	1406
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Qy	1407	CCTCACCCCAACCACTTAAACTGTCTATTGACATACAGAAATTAAGAAATTCATGTTGC	1466
Db	1725	CATGATCTCCTCCCTMAAGCGCTGCATCCGAGCTGTCCGAATTTCTACAGTTCCCTCTATA	1784
Qy	1467	AAAACGAAGTTTAAGAAAGCTTAACGTCATATGATATTAAGATATGTCATTGAAACATA	1526
Db	1785	TAAATAAAAGTTCAAGAGACGTTGAGGCTTTATGATGTGAAGATGTGATTGAGCACTA	1844
Qy	1527	TTCTGCTGGTATCTGCACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTTGATCA	1586
Db	1845	TTCCGCGCGGACATCTTGACATGCTTTCACAGATTAAGTACTTACAGACAAAGATATAT	1904
Qy	1587	AATTCCT 1592	
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; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

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Query Match 15.9%; Score 425; DB 3; Length 3287;

Best Local Similarity 64.7%; Pred. No. 1.2e-118;
Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0

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OY	124	GAGAGCCGCCGGGGCCAMGCAAGGGGGCCCGGATGAGCCCTGCTGGGGAAAGCCGCTCTTTAC	183
Db	187	GCCGGCTCCGAGGCGCCCCCAGCGGGGACAGACTCTTCAGCAAACTCCGCGGGCGGGCCG	246
OY	184	ACGAGTACCAGACTGCGGCGCGACGTCAGTACCGGCGGGTGCAGAACTACTCTGTAC	243
Db	247	GGCGCGGGAAAGCCCCCAACCGCAAGCCTTCTACCGCAAGCTGCAGAAATTTCTCTTAC	306
OY	244	AACGTGCTGAGABAAACCCCGGGGCTGGGCGCTTCAATCAACAGCTTTCGTTTTCTCCTT	303
Db	307	AACGTGCTGAGGCGGCGCGCGGCGCTGGGCGCTTCAATCAACAGCTTACTGTTCTCTG	366
OY	304	GCTCTTGGTTCCTGATTTTGTCACTGTCTTCTTCAATCCCTGAGCACACAAAATTGGCC	363
Db	367	GTTTTTCCTGCTCGTGGCTGTCTGTGTTTTCCACATCAAGAGTATGAGAAAGCTCG	426
OY	364	TCAAGTTCCTCTTGATCTTGGAGTTGGTATGATTTGTCTGCTTTTGGTTTGGATTATC	423
Db	427	GAGGGGGCCCTCTACATCTTGGAAATGCTGACTATCTGTGGTGTGGCGTGAATACCTTC	486
OY	424	ATTGGAATCTGTGTGCGGGTTCGTGTGTGTGATATAGAGATGGCAAGAACTGAGG	483
Db	487	GTGGGAACTTGGGCGGACAGGCTGCTGCTCGCGGTATCGTGGCTGAGAGGGGGCGGCTCAG	546
OY	484	TTTGCTGAAAAGCCCTTCTGTGTATATAGATACCAATTGTTCTTATGCTTCAATAGCAATT	543
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OY	604	CTACAGATCTCCGCATGTGTGCGATGACGATGACCCGAAGGGAGGCACTTGGAAATTACTGGGT	663
Db	667	CTGACGATTTCTGCGAGATGATCCGATGAGACCGCGGGGAGGCACTGGAACTCTGGGC	726
OY	664	TCAGTGGTTATGTCTCAGCAAGAAAGAAATTAATCAAGCTTGGTATAGATTTTGGTT	723
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OY	724	CTTATTTTTCGTTTCTTGTCTATCTGTGTGAAAAAGATGCCAAATMAAGATTTTCT	783
Db	787	CTATCTCTGGCCTCGTTCTGTGTGTACTTGGCAAGAAAGGGGAGAAAGCACTTTGTAC	846
OY	784	ACATATCCAGATGCTCTGTGTGGGGACAAATTATCTTGAACAATAATTTGGTATGAGAC	843
Db	847	ACCTACGGGATGACCTCTGTGTGGGCGCTGTATCAAGCTGACACACATTTGGCTTACGGGAC	906
OY	844	AAAACTCCCTTAATCTTGGCTGGGAAGATTGTTCTGCAAGCTTTGCACTCTTGGCAATT	903
Db	907	AAATACCCCCAGACTTGGAACGGGACGGCTCTTGCGGCAACTTCAACCTCATCGGTCTC	966
OY	904	TCTTTCTTTTGAATCTCTGCGCGGATCTTGGCTCAGATTTTGAATTAAGTACAAAGAA	963
Db	967	TCTCTTTCGGGCTGCGAGGATCTTGGGGCTGTGGTTTGGCTGAAAGTTTCAGAG	1026
OY	964	CAACACGGCCAGAAACTTTGAGAAAAGAAAGAACCCAGCTGCCAACTTCAATTCAGTGT	1023
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Page 17

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GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2662.2	99.8	3111	9	US-09-825-147-3
5	2662.2	99.8	3111	19	US-10-803-268-3
6	2630	98.6	2694	9	US-09-866-020-1
7	2630	98.6	2694	9	US-09-810-796-2

8	2630	98.6	2694	21	US-10-948-493-1	Sequence 1, Appli
9	2625.2	98.4	3071	9	US-09-810-796-1	Sequence 1, Appli
10	2625.2	98.5	3137	19	US-10-661-629-1	Sequence 1, Appli
11	2617.2	98.1	3074	9	US-09-813-148-1	Sequence 1, Appli
12	2617.2	98.1	3074	21	US-10-399-489A-5	Sequence 5, Appli
13	2615.6	98.1	3074	21	US-10-482-834A-55	Sequence 55, Appli
14	509.8	19.1	582	15	US-10-313-542-303	Sequence 303, App
15	492	18.4	2335	17	US-10-353-660-55	Sequence 55, Appli
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17	482	18.4	2335	21	US-10-399-489A-4	Sequence 4, Appli
18	489.2	18.3	2273	16	US-10-096-578-88	Sequence 88, Appli
19	475.6	17.8	2169	13	US-10-128-870-22	Sequence 22, Appli
20	475.6	17.8	2169	14	US-10-131-685-22	Sequence 22, Appli
21	475.2	17.8	2750	21	US-10-399-489A-2	Sequence 2, Appli
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25	472.2	17.7	7411	20	US-10-482-834A-59	Sequence 59, Appli
26	472.2	17.7	7411	20	US-10-335-053-6	Sequence 6, Appli
27	472.2	17.7	7420	17	US-10-295-027-281	Sequence 281, App
28	472.2	17.7	7420	20	US-10-643-785A-75	Sequence 75, Appli
29	472.2	17.7	7420	21	US-10-948-518-75	Sequence 75, Appli
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31	472.2	17.7	7863	15	US-10-084-817-335	Sequence 335, App
32	470.6	17.6	7407	21	US-10-482-834A-56	Sequence 56, Appli
33	465.4	17.5	896	13	US-10-128-870-1	Sequence 1, Appli
34	465.4	17.5	896	14	US-10-131-685-1	Sequence 1, Appli
35	465	17.4	548	10	US-09-826-73A-269	Sequence 269, App
36	452.2	17.0	7413	22	US-10-450-763-10636	Sequence 10636, A
37	452	16.9	575	15	US-10-313-542-305	Sequence 305, App
38	447	16.8	3195	22	US-10-450-763-10635	Sequence 10635, A
39	445.2	16.7	5595	19	US-10-820-307-8	Sequence 8, Appli
40	427.4	16.0	1848	20	US-10-744-796-5	Sequence 5, Appli
41	427.2	16.0	2665	13	US-10-128-870-26	Sequence 26, Appli
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43	427.2	16.0	2314	16	US-10-096-578-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1a1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 TACAAAGTGTGAGAGACCCGCGGCTGGGCTTATCTAACCGCTTTCGTTTTCTC 300
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QY 841 GACAAAACCTCCCTTAACCTTGTGTGGGAAATGCTTTCGAGGCTTTCACCTCTGGC 900
DB 841 GACAAAACCTCCCTTAACCTTGTGTGGGAAATGCTTTCGAGGCTTTCACCTCTGGC 900
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCAATCTTGTGGCTCAGGTTTTCATTAAGTACA 960
DB 901 ATTTCTTTCTTTGCACTTCTGCGGCAATCTTGTGGCTCAGGTTTTCATTAAGTACA 960
QY 961 GAAACAACACGCGCAGAAACATTTGAGAAAGAGAACCCAGCTGCCAACTCATTCG 1020
DB 961 GAAACAACACGCGCAGAAACATTTGAGAAAGAGAACCCAGCTGCCAACTCATTCG 1020
QY 1021 TGTGTTTGGCGTAGTACGAGCTGATGAGAAATCTGTTTCCATTGCCAATCTGGAAAGCA 1080
DB 1021 TGTGTTTGGCGTAGTACGAGCTGATGAGAAATCTGTTTCCATTGCCAATCTGGAAAGCA 1080

QY 1081 CACTTGAAGGCTTTCGACACCTTCAGCCCTTACCAATTCAGAAAGTAAAGTAAAGACGA 1140
DB 1081 CACTTGAAGGCTTTCGACACCTTCAGCCCTTACCAATTCAGAAAGTAAAGTAAAGACGA 1140
QY 1141 GTGGCAATGAGCTAAGCCCAAGGGGCGCAGAGTATTAAGACCCGACAGGCTCAGTAGTAC 1200
DB 1141 GTGGCAATGAGCTAAGCCCAAGGGGCGCAGAGTATTAAGACCCGACAGGCTCAGTAGTAC 1200
QY 1201 AGGAGTCCCAAGCAGCAGATCAGACCGAGGGCAGTCCCAACCAAGTGCAGAAAGAGC 1260
DB 1201 AGGAGTCCCAAGCAGCAGATCAGACCGAGGGCAGTCCCAACCAAGTGCAGAAAGAGC 1260
QY 1261 TGGAGCTTCAAGACCGAACCCTTCGCGCTCTGTGCGCTTCAAAAGTTCTACGCCA 1320
DB 1261 TGGAGCTTCAAGACCGAACCCTTCGCGCTCTGTGCGCTTCAAAAGTTCTACGCCA 1320
QY 1321 AAACGAGTATGATGATGCAACAGCCCTTGGGCACTGATGATGATGATGATGATGATGAT 1380
DB 1321 AAACGAGTATGATGATGCAACAGCCCTTGGGCACTGATGATGATGATGATGATGATGAT 1380
QY 1381 TGCAGTGTGATGATTCAGTGAAGACCTCACCCACCACTTAAACCTGTCAATTCGAGCT 1440
DB 1381 TGCAGTGTGATGATTCAGTGAAGACCTCACCCACCACTTAAACCTGTCAATTCGAGCT 1440
QY 1441 ATCAGAAATTAAGAAATTTTCATGTTGCAAAAGGAAATTTAAGAAACGTTTACGTCATAT 1500
DB 1441 ATCAGAAATTAAGAAATTTTCATGTTGCAAAAGGAAATTTAAGAAACGTTTACGTCATAT 1500
QY 1501 GATGTAAAGATGATGATGAAACAATATCTGTGCTCATCTGGAACATGTTGTGAAAT 1560
DB 1501 GATGTAAAGATGATGATGAAACAATATCTGTGCTCATCTGGAACATGTTGTGAAAT 1560
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DB 1561 AAAAGCTTCAAAACAGTGTGATCAAAATCTTGGAAAAAGGCAAAATCAGATCAGATTAAG 1620
QY 1621 AAGAGCCGAGGAAATTAACAGCAGAAATAGAGACCAAGACATCTCAGATGCTCGGT 1680
DB 1621 AAGAGCCGAGGAAATTAACAGCAGAAATAGAGACCAAGACATCTCAGATGCTCGGT 1680
QY 1681 CGGCTGTCAAGGTTGAAAAACAGGTACATCTGATAGAGTCCAACTGGAATGCTCACTA 1740
DB 1681 CGGCTGTCAAGGTTGAAAAACAGGTACATCTGATAGAGTCCAACTGGAATGCTCACTA 1740
QY 1741 GACATCTATCAACAGGCTCTTCGAAAGCTCTGCTCAGCCCTTGCTTGGCTTCATTC 1800
DB 1741 GACATCTATCAACAGGCTCTTCGAAAGCTCTGCTCAGCCCTTGCTTGGCTTCATTC 1800
QY 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGATCAAAAGCCCTGTGATAGCAAA 1860
DB 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGATCAAAAGCCCTGTGATAGCAAA 1860
QY 1861 GATCTTTCGGGTTCCGCAAAAACAGTGGCTTATCAGATCAACTAGTSCAAATTC 1920
DB 1861 GATCTTTCGGGTTCCGCAAAAACAGTGGCTTATCAGATCAACTAGTSCAAATTC 1920
QY 1921 TCGAAGGCTTCGAGTTCAATCTGACGCGCAATGATGATTCAGTGGCTTTCACGCG 1980
DB 1921 TCGAAGGCTTCGAGTTCAATCTGACGCGCAATGATGATTCAGTGGCTTTCACGCG 1980
QY 1981 CTTAAGCTTACTATGACAGTCAAGCAACAGAGTCCCAATTAATGATCAAAAGCATAGGCTCA 2040
DB 1981 CTTAAGCTTACTATGACAGTCAAGCAACAGAGTCCCAATTAATGATCAAAAGCATAGGCTCA 2040
QY 2041 GCAGTGGCAGCAACCAACCATTTGCAAAACCAATTAATTAATGAGGCAAGGCAAGCAGC 2100
DB 2041 GCAGTGGCAGCAACCAACCATTTGCAAAACCAATTAATTAATGAGGCAAGGCAAGCAGC 2100
QY 2101 CCAACCACTTTACAGATCCGACCTCTCCGAGCATCAAGCATCTGCCGAGGCGCAGAA 2160
DB 2101 CCAACCACTTTACAGATCCGACCTCTCCGAGCATCAAGCATCTGCCGAGGCGCAGAA 2160
QY 2161 ACTGTGACCCCTTAACCTTCGAGGCTTACAGGAAAGCATTTTCTGACGTACCACTGCTT 2220

Db	2161	ACTGTGCACCCTTAACCCCTGCAAGCTTTACAGAAAGCATTTTCTGACGTACCACTGCTT	2220
Qy	2221	GTTGCGCTCCAAAGAAATGTTTCAGGTTGCACAGTCAAACTTCACCCAAAGACGTTCTATG	2280
Db	2221	GTTGCGCTCCAAAGAAATGTTTCAGGTTGCACAGTCAAACTTCACCAAGACCGTTCTATG	2280
Qy	2281	AGGAAAGCTTTGACATGAGGAGAGAAACTCTGTGTTCTGTCTGTCCATGCTCCGAG	2340
Db	2281	AGGAAAGCTTTGACATGAGGAGAGAAACTCTGTGTTCTGTCTGTCCATGCTCCGAG	2340
Qy	2341	GACTTGCGCAAACTTTTGTCTGTGCAAAACCTGATCAGGTGACCCGAGAACTGAATATA	2400
Db	2341	GACTTGCGCAAACTTTTGTCTGTGCAAAACCTGATCAGGTGACCCGAGAACTGAATATA	2400
Qy	2401	CAACTTTGAGGAGTGAAGTCAAGTGCTCCAGAGCAGCAAGATTTTTCACCCAAATGG	2460
Db	2401	CAACTTTGAGGAGTGAAGTCAAGTGCTCCAGAGCAGCAAGATTTTTCACCCAAATGG	2460
Qy	2461	AGGGAATCCAAATTTGTTTATTAATCTGATGAAGAAGTGGGTCCCCGAAGACAGACAGAC	2520
Db	2461	AGGGAATCCAAATTTGTTTATTAATCTGATGAAGAAGTGGGTCCCCGAAGACAGACAGAC	2520
Qy	2521	ACTTTTGAATGCCGACCCGACAGCTGCCAGGGAAAGCTGTGTCATCGACCTCTCTAAG	2580
Db	2521	ACTTTTGAATGCCGACCCGACAGCTGCCAGGGAAAGCTGTGTCATCGACCTCTCTAAG	2580
Qy	2581	ACTGGAAGTCAAGATCATCTTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTC	2640
Db	2581	ACTGGAAGTCAAGATCATCTTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTC	2640
Qy	2641	AGCTTGCTCATGTCCAACTGAAATTA 2667	
Db	2641	AGCTTGCTCATGTCCAACTGAAATTA 2667	

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RESULT 2
US-09-825-147-1
? Sequence 1, Application US/09825147
? Patent No. US20020042505A1
? GENERAL INFORMATION:
? APPLICANT: Hu, Yi
? APPLICANT: Kieke, James Alvin
? APPLICANT: Turner, C. Alexander Jr.
? APPLICANT: Nehls, Michael C.
? APPLICANT: Friedrich, Glenn
? APPLICANT: Zambrowicz, Brian
? APPLICANT: Sands, Arthur T.
? TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
? FILE REFERENCE: LEX-0160-USA
? CURRENT APPLICATION NUMBER: US/09/825,147
? CURRENT FILING DATE: 2001-04-03
? PRIOR APPLICATION NUMBER: US 60/194,255
? PRIOR FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 2772
? TYPE: DNA
? ORGANISM: homo sapiens
US-09-825-147-1

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Query Match	99.8%	Score 2662.2	DB 9	Length 2772
Best Local Similarly	99.9%	Pred. No. 0		
Matches 2664	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

0y 1 ATGAAGGATGTGTGAATCCGGCCCGGGCCAGGGTGTCTGAACCTCCGACACCGCCAGGGGC 60
 Db 106 ATGAAGGATGTGTGAATCCGGCCCGGGCCAGGGTGTCTGAACCTCCGACACCGCCAGGGGC 165
 0y 61 GACGGCTGTCTACTGTGGGCAACCCGCGCGGACAGCTTGGTGTGGCGGCGGTGGCCCTG 120

Db	166	GACGGCCTGCTACTCTGCGGACACCCGCGCGGCACACGCTCGGTGGGCGGCGGTGGCCTG	225
Oy	121	AGGAGAGCCGCGCGGGGCAAGCAAGGAGGCCCGATGAGCTCTGCGGGAGCCGCTCTCT	180
Db	226	AGGAGAGAGCCGCGCGGGGCAAGCAAGGAGGCCCGATGAGCTCTGCGGGAGACCCCTCTCT	285
Oy	181	TACACGAGTACCGACAGCTGCGCGGCGCAACGTCAAGTACCGGCGGGTGCACATCACTG	240
Db	286	TACACGAGTACCGACAGCTGCGCGGCGCAACGTCAAGTACCGGCGGGTGCACATCACTG	345
Oy	241	TACACGAGTACCGACAGCTGCGCGGCGCAACGTCAAGTACCGGCGGGTGCACATCACTG	300
Db	346	TACACGAGTACCGACAGCTGCGCGGCGCAACGTCAAGTACCGGCGGGTGCACATCACTG	405
Oy	301	CTGTCTTTGGTTCCTTGATTTTGTCAAGTGTTCATCCATCCCTGAGACACAAAAATTG	360
Db	406	CTGTCTTTGGTTCCTTGATTTTGTCAAGTGTTCATCCATCCCTGAGACACAAAAATTG	465
Oy	361	GCCCTCAAGTTCCTCTTGATTCCTGGAGTTCGTATGATTCGTCTTTGGTTTGGAGTTC	420
Db	466	GCCCTCAAGTTCCTCTTGATTCCTGGAGTTCGTATGATTCGTCTTTGGTTTGGAGTTC	525
Oy	421	ATCATTTGGAATCTGAGTCGCGGGGTTGCTGTGTGATATAGAGATGGCAAGAAAGCTG	480
Db	526	ATCATTTGGAATCTGAGTCGCGGGGTTGCTGTGTGATATAGAGATGGCAAGAAAGCTG	585
Oy	481	AGTTTGTGTCGAAAGCCCTCTGTGTATATAGATCAATGTTCTTATCGCTTCAATAGCA	540
Db	586	AGTTTGTGTCGAAAGCCCTCTGTGTATATAGATCAATGTTCTTATCGCTTCAATAGCA	645
Oy	541	GTGTGTTTCTGCAAAAACCTCAGGGTAAATATTTTTCGCCAGTCTGCACTCAGAACTCCGT	600
Db	646	GTGTGTTTCTGCAAAAACCTCAGGGTAAATATTTTTCGCCAGTCTGCACTCAGAAAGTCCGT	705
Oy	601	TTCCTACAGATCCCTCCGATGAGTGGCATGAGACCGAAGGGAGGCACTGGAAATTACTG	660
Db	706	TTCCTACAGATCCCTCCGATGAGTGGCATGAGACCGAAGGGAGGCACTGGAAATTACTG	765
Oy	661	GGTTCAGTGGTTATGCTCACAGCAAGAAATTAATCAAGCTTGTAATAGATTTTGTG	720
Db	766	GGTTCAGTGGTTATGCTCACAGCAAGAAATTAATCAAGCTTGTAATAGATTTTGTG	825
Oy	721	GTCTCTATTTTTCGTCTTTCCTTGTCTATCTGAGTGAAGAAAGATGCCAATAAAGATT	780
Db	826	GTCTCTATTTTTCGTCTTTCCTTGTCTATCTGAGTGAAGAAAGATGCCAATAAAGATT	885
Oy	781	TCTACATATGAGATGCTCTCTGAGTGGGCAATATTCATTTGAACAATAATGGCTATAGCA	840
Db	886	TCTACATATGAGATGCTCTCTGAGTGGGCAATATTCATTTGAACAATAATGGCTATAGCA	945
Oy	841	GACAAAACCTCCCTAATCTTGAGTGGGAAGATGTCTTCTGCAAGCTTGTGCACTCCTTGGC	900
Db	946	GACAAAACCTCCCTAATCTTGAGTGGGAAGATGTCTTCTGCAAGCTTGTGCACTCCTTGGC	1005
Oy	901	ATTTCTTTCTTTGACATTCTCTGCGGGAATCTTGAGCTCAGGTTTGTGATTAAGTACAA	960
Db	1006	ATTTCTTTCTTTGACATTCTCTGCGGGAATCTTGAGCTCAGGTTTGTGATTAAGTACAA	1065
Oy	961	GAAACAACCGCCGCAAAACATTTGAGAAAAAGAAACCAAGCTGCCAACCCTATTACG	1020
Db	1066	GAAACAACCGCCGCAAAACATTTGAGAAAAAGAAACCAAGCTGCCAACCCTATTACG	1125
Oy	1021	TGTGTTTGGCGGTATTTAGCAGCTGATGAGAAATCTGTTCATTTGCACTGGAAAGCA	1080
Db	1126	TGTGTTTGGCGGTATTTAGCAGCTGATGAGAAATCTGTTCATTTGCACTGGAAAGCA	1185
Oy	1081	CACTTGAAAGGCTTGCACACCTGCAAGCCTTACCAATCAGAAAGCTTAAGTTTAAAGACGA	1140
Db	1186	CACTTGAAAGGCTTGCACACCTGCAAGCCTTACCAATCAGAAAGCTTAAGTTTAAAGACGA	1245
Oy	1141	GTGGGCAATGGCTTAAGCCCAAGGAGGCAAGATTTAAAGCCGCAAGACCTCAGTAGTGAC	1200
Db	1246	GTGGGCAATGGCTTAAGCCCAAGGAGGCAAGATTTAAAGCCGCAAGACCTCAGTAGTGAC	1305

QY	1201	AGGAGGTCCCCAAGACCGCAATCAACAGCCGAGGGCACTCCCAACAAAGTCAGAAAGC	1260
Db	1306	AGGAGGTCCCAAGACCGCAATCAACAGCCGAGGGCACTCCCAACAAAGTCAGAAAGC	1365
QY	1261	TGGAGCTTCAAAGACCGAACCCTTCCGGCCCTTGCTGCGCTCTAAAGTTCTCAAGCA	1320
Db	1366	TGGAGCTTCAAAGACCGAACCCTTCCGGCCCTTGCTGCGCTCTAAAGTTCTCAAGCA	1425
QY	1321	AAACCAAGATAGATGCTGACACAGCCCTTGACCTGATGATGATATGATGAAAGAAAGGA	1380
Db	1426	AAACCAAGATAGATGCTGACACAGCCCTTGACCTGATGATGATGATGATGAAAGAAAGGA	1485
QY	1381	TGCCAGTGTGATGTATCAGTGGAAAGCCTCAACCCCAACACTTTAAACCTGTATTCGAGCT	1440
Db	1486	TGCCAGTGTGATGTATCAGTGGAAAGCCTCAACCCCAACACTTTAAACCTGTATTCGAGCT	1545
QY	1441	ATCAGAATTATGAATTTCAATGTTGCAAAACGGAATTTAAAGAAACCTTACGTCCATAT	1500
Db	1546	ATCAGAATTATGAATTTCAATGTTGCAAAACGGAATTTAAAGAAACCTTACGTCCATAT	1605
QY	1501	GATGTAAGAAAGATGTCAATTGAACAAATATCTGCTGGTCATCTGGACATGTTGTGATGATT	1560
Db	1606	GATGTAAGAAAGATGTCAATTGAACAAATATCTGCTGGTCATCTGGACATGTTGTGATGATT	1665
QY	1561	AAAAACCTTCAAACACGTGTTGATCAAAATTTCTTGGAAAAAGGGCAAAATCAATCAGATPAG	1620
Db	1666	AAAAACCTTCAAACACGTGTTGATCAAAATTTCTTGGAAAAAGGGCAAAATCAATCAGATPAG	1725
QY	1621	AAGAGCCGAGAGAAATTAACAGCAAGAACATGAGACACAGACGATCTCAGATATGCTGGT	1680
Db	1726	AAGAGCCGAGAGAAATTAACAGCAAGAACATGAGACACAGACGATCTCAGATATGCTGGT	1785
QY	1681	CGGGTGTGCAAGGTTGTAAGAAAAACAGGTAACATCTCAGTCATAGAGTCCAAGCTGAGCTCTA	1740
Db	1786	CGGGTGTGCAAGGTTGTAAGAAAAACAGGTAACATCTCAGTCATAGAGTCCAAGCTGAGCTCTA	1845
QY	1741	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTC	1800
Db	1846	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTC	1905
QY	1801	CAGATCCCAACCTTTGGAATGTGAAACAGACATCTGACATCAAAAGCCCTGTGATAGAGAA	1860
Db	1906	CAGATCCCAACCTTTGGAATGTGAAACAGACATCTGACATCAAAAGCCCTGTGATAGAGAA	1965
QY	1861	GATCTTTTCGGGTTCCGCAAAAACAGTGGCTGCTTATTCAGATCAACCTAGTCCCAATC	1920
Db	1966	GATCTTTTCGGGTTCCGCAAAAACAGTGGCTGCTTATTCAGATCAACCTAGTCCCAATC	2025
QY	1921	TCGAGAGCCCTGACAGTTTCATCTGACCGCAAAATGAGTTCAATGATGCCAGACCTTTCTAACGC	1980
Db	2026	TCGAGAGCCCTGACAGTTTCATCTGACCGCAAAATGAGTTCAATGATGCCAGACCTTTCTAACGC	2085
QY	1981	CTTAGCCCTTACTATGACACAGTCAAGCAACAACAGGTGCCAATTAATGTCAAAGGATGGCTCA	2040
Db	2086	CTTAGCCCTTACTATGACACAGTCAAGCAACAACAGGTGCCAATTAATGTCAAAGGATGGCTCA	2145
QY	2041	GCACTGGCAGCCACCAACACCATTTGCAAAACCAATTAATACGACCCCAAGCCGACGACC	2100
Db	2146	GCACTGGCAGCCACCAACACCATTTGCAAAACCAATTAATACGACCCCAAGCCGACGACC	2205
QY	2101	CCAACCACTTTAGAGATCCCAACCTTCCTGCCACGANTCAAGATCTGCGCAGGCCAGAA	2160
Db	2206	CCAACCACTTTAGAGATCCCAACCTTCCTGCCACGANTCAAGATCTGCGCAGGCCAGAA	2265
QY	2161	ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAGCAATTTCTGAAGTCAACCACTGTGCTT	2220
Db	2266	ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAGCAATTTCTGAAGTCAACCACTGTGCTT	2325
QY	2221	GTTGCCCTTCAAGGAAAAATGTTCAAGTTGACACATGTCACCAAGACCGTTCTATG	2280
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[illegible]

RESULT 3
US-10-803-268-1

; Sequence 1, Application US/10803268
; Publication No. US20040157259A1

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; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
;

```

APPLICANT: Kiege, James Alvin
APPLICANT: Turner, C. Alexander J
APPLICANT: Noble, Michael C

APPLICANT: Zambronicz, Brian

APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human

FILE REFERENCE: LEX-0160-USA

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; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2004-03-18

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PRIOR APPLICATION NUMBER: US/09/82
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/10

; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: US 80/13
 ; NUMBER OF SEQ ID NOS: 3

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Vers
; SEQ ID NO 1

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;      LENGTH: 2772
;      TYPE: DNA
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;
US-10-803-268-1

Query Match	Score
99.8%	Score

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Best Local Similarity 99.9%; Pre
Matches 2664; Conservative 0;
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Db 106 ATGAGGATGTGAGTCGGGCGG

QY 61 GACGGCCTGCTACTGCTGGGCA

Db 166 GACGGCTGCTACTGCTGGGCAC

QY 121 AGGAGAGCCGCCGGGCAAGCA
 |||||
 Db 326 ACCGACACCGCCGCGGCAAGCA

226 AGGAGAGACCCGCGGGGCAAGCAGGGGGCCCGATGACCTGCTGGGGGAAGCCGCTCTT 285

Query Match 99.8%; Score 2662.2; DB 19; Length 2772.

Best Local Similarity	99.9%	Pred. No.	0
Matches 2664	Conservative	0	Mismatches 3
		Indels	0
		Gaps	0

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Db 106 ATGAAGATGAGATCGGCGCGGCGCAAGGTGCTGCTGAAC TCGGACGCCCGCAGGGGC 165

61 GACGGCCTGTACTGCTGGGCAACCGCGGCGACGCTTGTGTGGCGGCGGCTGACCTG 120

Db 166 GACGGCTGCTACTGCTGGGCAACCGCGGCAACGCTCGGTGGCGGCGGCGGCTG 225

121 AGGAGAGACCGCCGGGCAAGCAGGGGGCCGGATGAGCTGCTGGGGAGACCGCTCTT 180

226 AGGAGAGACCCGCCCGGCAAGCAGGGGGCCCCCGGATGAGCTCTGCTGGGGAAGCCGCTCTCT 285

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 Db 286 TACACGATGACGAGAGCTCCGGCGCAAGTCAAGTACCGGGGTGAGAACTACCTG 345
 QY 241 TACACGATGACGAGAGCTCCGGCGCAAGTCAAGTACCGGGGTGAGAACTACCTG 300
 Db 346 TACACGATGACGAGAGCTCCGGCGCAAGTCAAGTACCGGGGTGAGAACTACCTG 405
 QY 301 CTGTGCTTTGGTGTGATTTTGTGAGTGTTCATACCATCCCTGAGCAACAAATTG 360
 Db 406 CTGTGCTTTGGTGTGATTTTGTGAGTGTTCATACCATCCCTGAGCAACAAATTG 465
 QY 361 GCCTCAAGTTGCTCTGATCTGAGATTGCTGATGATGTCCTGTTGGTTGAGTTG 420
 Db 466 GCCTCAAGTTGCTCTGATCTGAGATTGCTGATGATGTCCTGTTGGTTGAGTTG 525
 QY 421 ATCATTCGAATCTGCTGCGGGTCTGTTGCTGATATAGAGATGGCAAGAGACTG 480
 Db 526 ATCATTCGAATCTGCTGCGGGTCTGTTGCTGATATAGAGATGGCAAGAGACTG 585
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 QY 601 TTCTCAAGATCTCCGCGATGCTGCGCATGAGCCGAAGGGAGGCACTTGAAATTAATG 660
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 Db 826 GTTCTAATTTTTCGTTCTTCTCTGTCTATCTGTGGAAGAAAGATCCCAATAAGAGTT 885
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 Db 886 TCTACATATGAGAGATCTCTGTGTGGGGGCAAAATTAATGAACAATATGCTATGGA 945
 QY 841 GACAAAACCTCCCTAATCTTGGCTGGGAAGATGCTTTCTGACAGCTTTGCACTCTTGGC 900
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 Db 1006 ATTTCTTTCTTTGCACTTCTGCGGCAATTTGCTCAGGTTTTCATTTAAAGATACA 1065
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 QY 1021 TGTGTTTGGCGTATAGCAAGTGTATGAGAAATCTGTTTCAATTGCAACTGGAAGCA 1080
 Db 1126 TGTGTTTGGCGTATAGCAAGTGTATGAGAAATCTGTTTCAATTGCAACTGGAAGCA 1185
 QY 1081 CACTTGAAGGCTTGGCAGACTGCAAGCTTACCAATCAGAAAGTATGTTTAAAGAGCA 1140
 Db 1186 CACTTGAAGGCTTGGCAGACTGCAAGCTTACCAATCAGAAAGTATGTTTAAAGAGCA 1245
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 Db 1246 GTTGCATGAGCTTAGCCCCAGGGGCGAGAGTATTAAGAGCCGACAGCTCAGTAGTAC 1305
 QY 1201 AGGAGGTCCCAAGCAACGACATCAAGCCGAGGGAGTCCCAACCAATTCAGAAAGAC 1260
 Db 1306 AGGAGGTCCCAAGCAACGACATCAAGCCGAGGGAGTCCCAACCAATTCAGAAAGAC 1365

QY 1261 TGGAGCTTCAAGCAACCGAAACCGCTTCGCGCCCTGCTGCGCTCAAAAGTTCTCAGCA 1320
 Db 1366 TGGAGCTTCAAGCAACCGAAACCGCTTCGCGCCCTGCTGCGCTCAAAAGTTCTCAGCA 1425
 QY 1321 AAAACGATATGATGCTGACACAGCCTTGGCACTGATGATGATATGATGAAAAAGGA 1380
 Db 1426 AAAACGATATGATGCTGACACAGCCTTGGCACTGATGATGATGATGAAAAAGGA 1485
 QY 1381 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 Db 1486 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1545
 QY 1441 ATCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1546 ATCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 QY 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Db 1606 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1665
 QY 1561 AAAAGCTTCAAGCAACCGTGTGATGATGATGATGATGATGATGATGATGATG 1620
 Db 1666 AAAAGCTTCAAGCAACCGTGTGATGATGATGATGATGATGATGATGATGATG 1725
 QY 1621 AAGAGCCGAGAGAAATAACAGCAACATGAGACCAAGAGATCTCAGTAGTCCGCT 1680
 Db 1726 AAGAGCCGAGAGAAATAACAGCAACATGAGACCAAGAGATCTCAGTAGTCCGCT 1785
 QY 1681 CCGGTGTCAAGGTTGAAAAACAGGTACATGATGATGATGATGATGATGATGATG 1740
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 QY 1741 GACATCTATCAACAGGCTCTTGGAAAGGCTGCTGCAAGCCCTGCTTGGCTTCAATC 1800
 Db 1846 GACATCTATCAACAGGCTCTTGGAAAGGCTGCTGCAAGCCCTGCTTGGCTTCAATC 1905
 QY 1801 CAGATCCCACTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1860
 Db 1906 CAGATCCCACTTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1965
 QY 1861 GATCTTTGGGGTTCGCGCAAAAAACAGTGGCTGCTTATCCAGATCAATGATGCAATC 1920
 Db 1966 GATCTTTGGGGTTCGCGCAAAAAACAGTGGCTGCTTATCCAGATCAATGATGCAATC 2025
 QY 1921 TCGAAGGCTGCAAGTATCTGACGCCAATGAGTTCAAGTCCCACTTCTGATGCGG 1980
 Db 2026 TCGAAGGCTGCAAGTATCTGACGCCAATGAGTTCAAGTCCCACTTCTGATGCGG 2085
 QY 1981 CTTAGCCCTCATATGACAGTCAAGCAACACAGTGGCAATTAATGATGATGATGATG 2040
 Db 2086 CTTAGCCCTCATATGACAGTCAAGCAACACAGTGGCAATTAATGATGATGATGATG 2145
 QY 2041 GCAGTGGAGCCCAACACATTTGCAAAACCAATTAATGAGGACCAAGCCAGCAGCC 2100
 Db 2146 GCAGTGGAGCCCAACACATTTGCAAAACCAATTAATGAGGACCAAGCCAGCAGCC 2205
 QY 2101 CCAACAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
 Db 2206 CCAACAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2265
 QY 2161 ACTGTGACCCCTTAACCTGAGAGGCTTACAGGAAAGCATTTTGAAGTCAACCACTGCTT 2220
 Db 2266 ACTGTGACCCCTTAACCTGAGAGGCTTACAGGAAAGCATTTTGAAGTCAACCACTGCTT 2325
 QY 2221 GTTGCCTTCAAGAAATGTTTCAAGTTCACAAATTTTCAACAGGACCGTTCTATG 2280
 Db 2326 GTTGCCTTCAAGAAATGTTTCAAGTTCACAAATTTTCAACAGGACCGTTCTATG 2385
 QY 2281 AGGAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 Db 2386 AGGAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2445
 QY 2341 GACTTGGGCAAAATCTTGTCTGTGCAAAACCTGATCAGTGGACCGAGAACTGATATA 2400

Db 2446 GACTTGGGAAAACCTTGTCTGTGCAAAACCTGATCAGTCGACCGAGAACTGAAATATA 2505
Qy 2401 CAACCTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACGCAAGATTTTACCCTAAATGG 2460
Db 2506 CAACCTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACGCAAGATTTTACCCTAAATGG 2565
Qy 2461 AGGGAATCCAAATTTTAACTGATGAAGAAGTGGTCCGAGAGACAGAGACAGAC 2520
Db 2566 AGGGAATCCAAATTTTAACTGATGAAGAAGTGGTCCGAGAGACAGAGACAGAC 2625
Qy 2521 ACTTTGATGCGCGACGCGAGCTGCGAGGAAAGCTGCTTGGATCAGACTCTCTAAG 2580
Db 2626 ACTTTGATGCGCGACGCGAGCTGCGAGGAAAGCTGCTTGGATCAGACTCTCTAAG 2685
Qy 2581 ACTGAAGTCAAGATCATCTCAGAGCATTTTGAAGGACAGAAAGTACAGATGCCCTC 2640
Db 2686 ACTGAAGTCAAGATCATCTCAGAGCATTTTGAAGGACAGAAAGTACAGATGCCCTC 2745
Qy 2641 AGCTTGCTCATGTCAAACTGAAATTA 2667
Db 2746 AGCTTGCTCATGTCAAACTGAAATTA 2772

RESULT 4
US-09-825-147-3
Sequence 3, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu. Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
FILE REFERENCE: Polynucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US/09/825,147
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-3

Query Match 99.8%; Score 2662.2; DB 9; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAAGAGATGTGAGTTCGGGCGGAGGAGGAGTGTCTGTAACCTCGGACGCGCAGGGGC 60
Db 165 ATGAAGAGATGTGAGTTCGGGCGGAGGAGGAGTGTCTGTAACCTCGGACGCGCAGGGGC 224
Qy 61 GACGGCTGTCTAATGCTGGGCAACCGGCGGCGACGCTGTGTGGGCGGCGGTGGCCCTG 120
Db 225 GACGGCTGTCTAATGCTGGGCAACCGGCGGCGACGCTGTGTGGGCGGCGGTGGCCCTG 284
Qy 121 AGGAGAGCGCGCGGAGCAAGAGGAGGCGCGGATGAGCTGTGGGAAAGCGCTCTCT 180
Db 285 AGGAGAGCGCGCGGAGCAAGAGGAGGCGCGGATGAGCTGTGGGAAAGCGCTCTCT 344
Qy 181 TACACGATGATGACGAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCAAACTAATCTG 240
Db 345 TACACGATGATGACGAGCTGCGGCGCAACGTCAAGTACCGGCGGTGCAAACTAATCTG 404
Qy 241 TACAAGTGTGAGAGATCCCGGCGGTGAGCTTATACACGCTTTCTTTTCTC 300

Db 405 TACAAGTGTGAGAGATCCCGGCGGTGAGCTTATACACGCTTTGTTTTCTC 464
Qy 301 CTGTGCTTGGTGGTGAATTTTGTCAAGTGTCTTACATCCCTGACACAAATATG 360
Db 465 CTGTGCTTGGTGGTGAATTTTGTCAAGTGTCTTACATCCCTGACACAAATATG 524
Qy 361 GCTCAAGTGGCTTTTATCTGTGAGTTCGTATGATTTGTCGTTTGGTTGAGTTTC 420
Db 525 GCTCAAGTGGCTTTTATCTGTGAGTTCGTATGATTTGTCGTTTGGTTGAGTTTC 584
Qy 421 ATCATTCGAATCTGTGTCGCGGTTGCTGTGTGATATAGAGATGAGGCAAGAACTG 480
Db 585 ATCATTCGAATCTGTGTCGCGGTTGCTGTGTGATATAGAGATGAGGCAAGAACTG 644
Qy 481 AGGTTTGTGAAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
Db 645 AGGTTTGTGAAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 704
Qy 541 GTTGTGTTCTGAAAACCTCAGGTTAATTTTGTGACGTCGCACTCAGAACTCCGT 600
Db 705 GTTGTGTTCTGAAAACCTCAGGTTAATTTTGTGACGTCGCACTCAGAACTCCGT 764
Qy 601 TTCTACAGATCTCCGATGCTGCGCATGAGACCGAAGGAGGACCTGAAATTAATCTG 660
Db 765 TTCTACAGATCTCCGATGCTGCGCATGAGACCGAAGGAGGACCTGAAATTAATCTG 824
Qy 661 GGTTCAGTGTGTTATGCTCAGACGAGAAATTAATCAGCTGTGTACATAGATTTTGTG 720
Db 825 GGTTCAGTGTGTTATGCTCAGACGAGAAATTAATCAGCTGTGTACATAGATTTTGTG 884
Qy 721 GTTCTTATTTTGTGCTTCTTCTGTGCTATCTGTGTGAAAAGATGCCAATTAAGATTT 780
Db 885 GTTCTTATTTTGTGCTTCTTCTGTGCTATCTGTGTGAAAAGATGCCAATTAAGATTT 944
Qy 781 TCTACATATGAGATGCTCTGCGGAGGCAAAATTAATGACAACTATTGCTATGGA 840
Db 945 TCTACATATGAGATGCTCTGCGGAGGCAAAATTAATGACAACTATTGCTATGGA 1004
Qy 841 GACAAATCCCTTAACCTTGTGAGAAATTTCTTGTGAGGCTTGTGACCTCTTGGC 900
Db 1005 GACAAATCCCTTAACCTTGTGAGAAATTTCTTGTGAGGCTTGTGACCTCTTGGC 1064
Qy 901 ATTTCTTCTTGTGACCTTCTGCGGCAATTTCTGTGCTAGGTTTGTGCAATTAAGTACA 960
Db 1065 ATTTCTTCTTGTGACCTTCTGCGGCAATTTCTGTGCTAGGTTTGTGCAATTAAGTACA 1124
Qy 961 GAACAAACCGCGCAAGAACTTTGAGAAAAGAAAGAACCCAGCTGCAACCTCATTCAG 1020
Db 1125 GAACAAACCGCGCAAGAACTTTGAGAAAAGAAAGAACCCAGCTGCAACCTCATTCAG 1184
Qy 1021 TGTGTTTGGGTAGTTAGCAGCTGATGAGAAATCTGTTTCATTTGCAACTGGAAGCCA 1080
Db 1185 TGTGTTTGGGTAGTTAGCAGCTGATGAGAAATCTGTTTCATTTGCAACTGGAAGCCA 1244
Qy 1081 CACTTGAAGGCTTGTGCAACCTGCAAGCCCTTACATCAAGGCTTAAGTTTAAAGAGGA 1140
Db 1245 CACTTGAAGGCTTGTGCAACCTGCAAGCCCTTACATCAAGGCTTAAGTTTAAAGAGGA 1304
Qy 1141 GTGCGATGCTAGGCGCGGAGGCGCAAGTATTAAGAGCCGCAAGCTCAGTAGTAC 1200
Db 1305 GTGCGATGCTAGGCGCGGAGGCGCAAGTATTAAGAGCCGCAAGCTCAGTAGTAC 1364
Qy 1201 AGAGAGTCCCAAGACCGACATCAACAGCGAGGCACTCCACCAAGTGCAGAAAGGC 1260
Db 1365 AGAGAGTCCCAAGACCGACATCAACAGCGAGGCACTCCACCAAGTGCAGAAAGGC 1424
Qy 1261 TGAAGTTCAACGACCAACCCGCTTCCGCGCTTCTGCGCCCTCAAAAGTTTCAAGCA 1320
Db 1425 TGAAGTTCAACGACCAACCCGCTTCCGCGCTTCTGCGCCCTCAAAAGTTTCAAGCA 1484
Qy 1321 AAACAGTATAGATGCTGACACAGCCCTTGGACCTGATGATATATGATGAAAAAGGA 1380
Db 1485 AAACAGTATAGATGCTGACACAGCCCTTGGACCTGATGATATATGATGAAAAAGGA 1544

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Qy 1381 TGGCAGTGTATGATATGATGAGAGACCTGACCCCACTTAAAACTGTCATTGAGCT 1440
Db 1545 TGGCAGTGTATGATATGATGAGAGACCTGACCCCACTTAAAACTGTCATTGAGCT 1604
Qy 1441 ATCAAAATTAATGAAATTTTATGTTTGAAGAAAGGAAATTTAAAGAAAGGAAATTTTAAAG 1500
Db 1605 ATCAAAATTAATGAAATTTTATGTTTGAAGAAAGGAAATTTAAAGAAAGGAAATTTTAAAG 1664
Qy 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1665 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724
Qy 1561 AAAAGCTTGAACACGCTGTTGATCAATTTCTTGAAAAAGGCAAAATCATCATGATGATGATGAT 1620
Db 1725 AAAAGCTTGAACACGCTGTTGATCAATTTCTTGAAAAAGGCAAAATCATCATGATGATGATGAT 1784
Qy 1621 AAGAGCCGAGAGAAATTAACAGCAAAATGAGACCAAGATGATGATGATGATGATGATGATGATGAT 1680
Db 1785 AAGAGCCGAGAGAAATTAACAGCAAAATGAGACCAAGATGATGATGATGATGATGATGATGATGAT 1844
Qy 1681 CGGGTGTCAAGGTGTAAGAAACAGGTACAGTCCATAGAGTCAAGCTGATGATGATGATGATGATGAT 1740
Db 1845 CGGGTGTCAAGGTGTAAGAAACAGGTACAGTCCATAGAGTCAAGCTGATGATGATGATGATGATGAT 1904
Qy 1741 GACATCTATCAACAGGTCTTTCGAAAGGCTTGCCTCAGCCCTCGCTTGGCTTCAATTC 1800
Db 1905 GACATCTATCAACAGGTCTTTCGAAAGGCTTGCCTCAGCCCTCGCTTGGCTTCAATTC 1964
Qy 1801 CAGATCCACCTTTTGAATGTAACAGACATCTGATCAATCAAAAGCTGATGATGATGATGATGATGAT 1860
Db 1965 CAGATCCACCTTTTGAATGTAACAGACATCTGATCAATCAAAAGCTGATGATGATGATGATGATGAT 2024
Qy 1861 GATCTTTCGGGTTCCGCAAAACAGGCTGCTTATCCAGATCAATCAATGATGATGATGATGATGATGAT 1920
Db 2025 GATCTTTCGGGTTCCGCAAAACAGGCTGCTTATCCAGATCAATCAATGATGATGATGATGATGATGAT 2084
Qy 1921 TCGAGAGGCTGAGTTCATTTGACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 2085 TCGAGAGGCTGAGTTCATTTGACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2144
Qy 1981 CTTAGCCCTACTATGACAGTCAAGCAACAGGTGCTCAATGATCAAGCAAGTATGATGATGATGATGAT 2040
Db 2145 CTTAGCCCTACTATGACAGTCAAGCAACAGGTGCTCAATGATCAAGCAAGTATGATGATGATGATGAT 2204
Qy 2041 GCAGTGGCAACCCCAACCAATTTGCAACCAATTAATACGGAACCCCAAGCCAGCC 2100
Db 2205 GCAGTGGCAACCCCAACCAATTTGCAACCAATTAATACGGAACCCCAAGCCAGCC 2264
Qy 2101 CCAACAACTTTAAGATCCCACTCTCTCCAGCCATCAAGCATGTCGCCAGGCGCAGAA 2160
Db 2265 CCAACAACTTTAAGATCCCACTCTCTCCAGCCATCAAGCATGTCGCCAGGCGCAGAA 2324
Qy 2161 ACTTCGACCCCTTAACCTTCGAGGCTTACAGAAAGCATTTTCTGACGTCAACCTGCTCT 2220
Db 2325 ACTTCGACCCCTTAACCTTCGAGGCTTACAGAAAGCATTTTCTGACGTCAACCTGCTCT 2384
Qy 2221 GTTTCCTCCCAAGAAATTTTCAAGTTCACAGTCAAAATCTCAACCAAGGACGTTCTATG 2280
Db 2385 GTTTCCTCCCAAGAAATTTTCAAGTTCACAGTCAAAATCTCAACCAAGGACGTTCTATG 2444
Qy 2281 AGGAAAAAGCTTTGACATGAGAGAGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2445 AGGAAAAAGCTTTGACATGAGAGAGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2504
Qy 2341 GACTTGGGCAAAATTTTGTCTGTGCAAAACCTGATCAGGTCAACCGAGAACTGAATATA 2400
Db 2505 GACTTGGGCAAAATTTTGTCTGTGCAAAACCTGATCAGGTCAACCGAGAACTGAATATA 2564
Qy 2401 CAATCTTCAAGGAGTGAAGTGAAGTCTCAAGGCAAGCCCAATTTTCAATTTTCAATTTTCAATTTTCA 2460
Db 2565 CAATCTTCAAGGAGTGAAGTGAAGTCTCAAGGCAAGCCCAATTTTCAATTTTCAATTTTCAATTTTCA 2624
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Qy 2461 AGGAAATCCAAATTTGTTTAACTGATGAAGAGTGGTCCGGAAGAGACAGAGACAGAC 2520
Db 2625 AGGAAATCCAAATTTGTTTAACTGATGAAGAGTGGTCCGGAAGAGACAGAGACAGAC 2684
Qy 2521 ACTTTGATGCGGACACCGACGCTGCGAGGAAAGCTGCTTTGATCAAGCTCTTAAG 2580
Db 2685 ACTTTGATGCGGACACCGACGCTGCGAGGAAAGCTGCTTTGATCAAGCTCTTAAG 2744
Qy 2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGCAAGAAATGACAGATGCGCTTC 2640
Db 2745 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGCAAGAAATGACAGATGCGCTTC 2804
Qy 2641 AGCTTCCTCATGTCAAACTGAAATTA 2667
Db 2805 AGCTTCCTCATGTCAAACTGAAATTA 2831

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kleke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 99.8%; Score 2662.2; DB 19; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAAGAGTGTGAAGTCCGGGCGGAGGAGGCTGCTGAACCTCGGACGCGCGAGGGGC 60
Db 165 ATGAAGAGTGTGAAGTCCGGGCGGAGGAGGCTGCTGAACCTCGGACGCGCGAGGGGC 224
Qy 61 GACGCGCTGCTACTGCTGCGGACACCGCGCGGACGCTTGTGTGCGGCGGCGGCTCTG 120
Db 225 GACGCGCTGCTACTGCTGCGGACACCGCGCGGACGCTTGTGTGCGGCGGCGGCTCTG 284
Qy 121 AGGAGAGCGCGCGGCGGCAAGCAAGGAGCGCGGATGAGCTGCTGAGGAAAGCGCTCT 180
Db 285 AGGAGAGCGCGCGGCGGCAAGCAAGGAGCGCGGATGAGCTGCTGAGGAAAGCGCTCT 344
Qy 181 TACAGAGTGAAGCAGAGCTGCGGCGCAACGTCAGTACCGGCGGCTGAGAACTAACCTG 240
Db 345 TACAGAGTGAAGCAGAGCTGCGGCGCAACGTCAGTACCGGCGGCTGAGAACTAACCTG 404
Qy 241 TACAACTGCTGAGAGAGACCCCGCGGCTGAGGCTTCACTCAACAGCTTTGCTTTCTC 300
Db 405 TACAACTGCTGAGAGAGACCCCGCGGCTGAGGCTTCACTCAACAGCTTTGCTTTCTC 464
Qy 301 CTGTCTCTTGTGCTGCTGATTTTGTGATGATTTTCTACCATCTCTGAGACACAAATTG 360
Db 465 CTGTCTCTTGTGCTGCTGATTTTGTGATGATTTTCTACCATCTCTGAGACACAAATTG 524
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QY 361 GCCTCAAGTTGACCTTGTATCTGAGATTGATGATGTCGTTGTTGGATTG 420
 Db 525 GCCTCAAGTTGACCTTGTATCTGAGATTGATGATGTCGTTGTTGGATTG 584
 QY 421 ATGATTCGAATCTGATCTGGGGTGTGTGTCATATGAGATGCGAAGAACTG 480
 Db 585 ATGATTCGAATCTGATCTGGGGTGTGTGTCATATGAGATGCGAAGAACTG 644
 QY 481 AGGTTGCTGGAAGCCCTCTGTATATGATACCATGTTCTTATGCTTCAATAGA 540
 Db 645 AGGTTGCTGGAAGCCCTCTGTATATGATACCATGTTCTTATGCTTCAATAGA 704
 QY 541 GTTGTGTTGCAAAAATCTCAGGGTAAATATTTTGGCAAGCTTGCACTCAGAACTCCGT 600
 Db 705 GTTGTGTTGCAAAAATCTCAGGGTAAATATTTTGGCAAGCTTGCACTCAGAACTCCGT 764
 QY 601 TTCTCTACAGATCTCTCCGATGATGCGCATGACCGAAGGGGAGGCACTTGAATTAATCTG 660
 Db 765 TTCTCTACAGATCTCTCCGATGATGCGCATGACCGAAGGGGAGGCACTTGAATTAATCTG 824
 QY 661 GGTTCAAGGTTATGCTCAGCAGAGAAATTAATCAAGCTTGATACATAGGATTTTGG 720
 Db 825 GGTTCAAGGTTATGCTCAGCAGAGAAATTAATCAAGCTTGATACATAGGATTTTGG 884
 QY 721 GTTCTTATTTTTCGTCTTTCCTTGTCTATCTGTGGAAGAAAGGATGCCAATAAGAGTTT 780
 Db 885 GTTCTTATTTTTCGTCTTTCCTTGTCTATCTGTGGAAGAAAGGATGCCAATAAGAGTTT 944
 QY 781 TCTACATATGCAAGATCTCTGTGTGGGGGCAAAATTAATGACATATATGCTATGATG 840
 Db 945 TCTACATATGCAAGATCTCTGTGTGGGGGCAAAATTAATGACATATATGCTATGATG 1004
 QY 841 GACAAAATCTCCCTTAATGCTGAGGAGATGCTTTCGACAGGCTTTCACATCTCTGAGC 900
 Db 1005 GACAAAATCTCCCTTAATGCTGAGGAGATGCTTTCGACAGGCTTTCACATCTCTGAGC 1064
 QY 901 ATTTCTTTCTTTGACCTTCTGCGGCAATCTTGTGCTCAGGTTTTCATTTAAAGTACAA 960
 Db 1065 ATTTCTTTCTTTGACCTTCTGCGGCAATCTTGTGCTCAGGTTTTCATTTAAAGTACAA 1124
 QY 961 GAACAACACCGCCAGAAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAATCTCATTCAG 1020
 Db 1125 GAACAACACCGCCAGAAAACATTTGAGAAAAGAAAGAACCCAGCTGCCAATCTCATTCAG 1184
 QY 1021 TGTGTTTGGCGTATGATCAGAGCTGATGAGAAATCTGTTCCATTCGACCTGGAAGCCA 1080
 Db 1185 TGTGTTTGGCGTATGATCAGAGCTGATGAGAAATCTGTTCCATTCGACCTGGAAGCCA 1244
 QY 1081 CACTTGAAGGCTTGCACACCTGACGCCCTTACCAATCAGAAAGTTAAAGAGCGA 1140
 Db 1245 CACTTGAAGGCTTGCACACCTGACGCCCTTACCAATCAGAAAGTTAAAGAGCGA 1304
 QY 1141 GTGCGATGAGCTAGCCCGAGGGGCGAGATTTAAAGCGGACAAAGCTCAGATGATGAC 1200
 Db 1305 GTGCGATGAGCTAGCCCGAGGGGCGAGATTTAAAGCGGACAAAGCTCAGATGATGAC 1364
 QY 1201 AGAAGGTTCCCAAGCAGCAGATCAGAGCGAGGAGTCCCAACAAATGCGAAGAGAC 1260
 Db 1365 AGAAGGTTCCCAAGCAGCAGATCAGAGCGAGGAGTCCCAACAAATGCGAAGAGAC 1424
 QY 1261 TGGAGCTTCAACGACCGAACCCGCTTCCGCGCTCGCTCGCTCAAAAAGTTCTCAGCCA 1320
 Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCCGCGCTCGCTCGCTCAAAAAGTTCTCAGCCA 1484
 QY 1321 AAACCGATATGATGCTGACACAGCCCTTGGACATGATGATATATGATGAAAAAGGA 1380
 Db 1485 AAACCGATATGATGCTGACACAGCCCTTGGACATGATGATATATGATGAAAAAGGA 1544
 QY 1381 TGGCAGTGTATGATCAGTGAAGACCTCACCCCACTTAAACCTGCTATTCGAGCT 1440
 Db 1545 TGGCAGTGTATGATCAGTGAAGACCTCACCCCACTTAAACCTGCTATTCGAGCT 1604

QY 1441 ATCAGAAATTAGAAAATTTTCATGTGGCAAAACGGAAGTTTAAAGAAAACGTATGTCATAT 1500
 Db 1605 ATCAGAAATTATGAAAATTTTCATGTGGCAAAACGGAAGTTTAAAGAAAACGTATGTCATAT 1664
 QY 1501 GATGTAAAAGATGTATGTAACAAATTTCTGTGTCTATCTGACATGTTGTGTGAATT 1560
 Db 1665 GATGTAAAAGATGTATGTAACAAATTTCTGTGTCTATCTGACATGTTGTGTGAATT 1724
 QY 1561 AAAAGCTTCAAAACAGTGTGATCAAAATCTTGGAAAAAGGCAAAATCAGATCAGATAAG 1620
 Db 1725 AAAAGCTTCAAAACAGTGTGATCAAAATCTTGGAAAAAGGCAAAATCAGATCAGATAAG 1784
 QY 1621 AAGACCCGAGAGAAAATTAACAGCAGACATGAGACACAGATCTCAGATATGCTGGGT 1680
 Db 1785 AAGACCCGAGAGAAAATTAACAGCAGACATGAGACACAGATCTCAGATATGCTGGGT 1844
 QY 1681 CCGGTGTGTCAAGTTGAAAAACAGGTACAGTCCATAGAGTCCAGAGTGGACTGCTACTTA 1740
 Db 1845 CCGGTGTGTCAAGTTGAAAAACAGGTACAGTCCATAGAGATCCAGAGTGGACTGCTACTTA 1904
 QY 1741 GACATCTATCAACAGGTCCTTTCGAAAAGGCTCTGAGCCCTGCTTGGCTTCAATTC 1800
 Db 1905 GACATCTATCAACAGGTCCTTTCGAAAAGGCTCTGAGCCCTGCTTGGCTTCAATTC 1964
 QY 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGAATTAACAAAGCCCTGTGATAGCAAA 1860
 Db 1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGAATTAACAAAGCCCTGTGATAGCAAA 2024
 QY 1861 GATCTTTGGGTTTCGCAAAAACAGTGGCTGTTATCCAGATCAATAGTGGCAACATC 1920
 Db 2025 GATCTTTGGGTTTCGCAAAAACAGTGGCTGTTATCCAGATCAATAGTGGCAACATC 2084
 QY 1921 TCGAAGGCTCGCAGTTTCAATCTGACGCGCAATGAGTTCACTGCGCAGACTTTCACGCG 1980
 Db 2085 TCGAAGGCTCGCAGTTTCAATCTGACGCGCAATGAGTTCACTGCGCAGACTTTCACGCG 2144
 QY 1981 CTTAGCCCTCAATGACAGTCAAGCAACACAGTGGCCCAATTAATGTAAGCGATGCTCA 2040
 Db 2145 CTTAGCCCTCAATGACAGTCAAGCAACACAGTGGCCCAATTAATGTAAGCGATGCTCA 2204
 QY 2041 GCAGTGGCAGCAACCAACCATGAGCAACCAATTAATGAGGACCCAGAGCAGACGCC 2100
 Db 2205 GCAGTGGCAGCAACCAACCATGAGCAACCAATTAATGAGGACCCAGAGCAGACGCC 2264
 QY 2101 CCAACCACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCAGGCGAGAA 2160
 Db 2265 CCAACCACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCAGGCGAGAA 2324
 QY 2161 ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAAGCATTTGTGACGTACCACTGCTT 2220
 Db 2325 ACTGTGACCCCTAACCCCTGACAGGCTTACAGAAAAGCATTTGTGACGTACCACTGCTT 2384
 QY 2221 GTTGGCTTCAAGAAAATGTTCAAGTTGCAAGTCAAAATCTCACCAAGAACCGTTCTATG 2280
 Db 2385 GTTGGCTTCAAGAAAATGTTCAAGTTGCAAGTCAAAATCTCACCAAGAACCGTTCTATG 2444
 QY 2281 AGAAGAACTTTGACATGAGGAGAGAACTCTGTTGTCTGTCTGTCCATGATGTCGGAAG 2340
 Db 2445 AGAAGAACTTTGACATGAGGAGAGAACTCTGTTGTGTCTGTCTGTCCATGATGTCGGAAG 2504
 QY 2341 GACTTTGGGCAAAATCTTTGTCTGTGCAAAAACCTGATCAGGTGACCGAGAACTGATATTA 2400
 Db 2505 GACTTTGGGCAAAATCTTTGTCTGTGCAAAAACCTGATCAGGTGACCGAGAACTGATATTA 2564
 QY 2401 CAACCTTGAAGGAGTGTCAAGTGGCTCCAGAGGCGCAAGATTTTACCCCAAAATGG 2460
 Db 2565 CAACCTTGAAGGAGTGTCAAGTGGCTCCAGAGGCGCAAGATTTTACCCCAAAATGG 2624
 QY 2461 AGGGAATCAAAATTTTATTAATCAGTGAAGAGTGGGTCCCGAAGACAGAGACAGAC 2520
 Db 2625 AGGGAATCAAAATTTTATTAATCAGTGAAGAGTGGGTCCCGAAGACAGAGACAGAC 2684
 QY 2521 ACTTTGATGCGGACCGCAGCCTGCGCAGGGAAGCTGCTTTGATCACTCTCTAAGG 2580

Db 2685 ACTTTGATGCGGACCGGAGCTGCGAGGGAGCTGCTTTCATGAGACTCTTAAGG 2744
Qy 2581 ACTGGAAGTCAGCATATCTCAAGCATTTTGAAGCAGAGAAAGTACAGATGCCCTC 2640
Db 2745 ACTGGAAGTCAGCATATCTCAAGCATTTTGAAGCAGAGAAAGTACAGATGCCCTC 2804
Qy 2641 AGCTTGCTCATGTCAAACTGAATTA 2667
Db 2805 AGCTTGCTCATGTCAAACTGAATTA 2831

RESULT 6
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOPF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

Qy 1 ATGAAGATGTGAGTGGGCGGCGGAGAGGTGCTGTGAACCTGCGAGCGCGCCAGGGGC 60
Db 1 ATGAAGATGTGAGTGGGCGGCGGAGAGGTGCTGTGAACCTGCGAGCGCGCCAGGGGC 60
Qy 61 GAGGCGCTGTACTGCTGTGGGCAACCGCGGCGGCAAGCTTGTGGCGGCGGCGGCTGTG 120
Db 61 GAGGCGCTGTACTGCTGTGGGCAACCGCGGCGGCAAGCTTGTGGCGGCGGCGGCTGTG 120
Qy 121 AGGGAAGCGCGCGGCGGCAAGAGGGGGCGGATGAGCTGTGCGGGAAGCGGCTCTT 180
Db 121 AGGGAAGCGCGCGGCGGCAAGAGGGGGCGGATGAGCTGTGCGGGAAGCGGCTCTT 180
Qy 181 TACACGATGAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGATGAGAACTAACCTG 240
Db 181 TACACGATGAGCAGAGCTGCGGCGCAACGTCAAGTACCGGCGGATGAGAACTAACCTG 240
Qy 241 TACAACTGCTGAGAGAACCCCGGCGGCTGAGCTTCACTAACACGCTTTTCTTC 300
Db 241 TACAACTGCTGAGAGAACCCCGGCGGCTGAGCTTCACTAACACGCTTTTCTTC 300
Qy 301 CTGTCTTTGGTGTGCTGATTTTGTCAAGTCTTCAACATCCCTGAGCACAATAATTG 360
Db 301 CTGTCTTTGGTGTGCTGATTTTGTCAAGTCTTCAACATCCCTGAGCACAATAATTG 360
Qy 361 GCTCTCAAGTGTCTTGTGATCTGAGATCTGATGATGATGATGATGATGATGATGATG 420
Db 361 GCTCTCAAGTGTCTTGTGATCTGAGATCTGATGATGATGATGATGATGATGATGATG 420
Qy 421 ATCATTTGAAATCTGCTGCGGGGTGCTGTGCTGATATAGAGATGCGCAAGAAAGCTG 480
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Qy 481 AGGTTTCTGAAAGCCCTCTGTGTTATAGATACCATTTGTTTCAATGCAATAGCA 540
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Qy 661 GGTTCAGTGTGTTATGCTCAGACAGAAATTAATCAAGCTTGTGATAGATTTTGG 720
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Qy 1116 --TCAGAGCTAAGTTTAAAGAGCGAGTGCATGAGCCCGAGGGCCAGATATT 1173
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QY 1894 TTATCCAGATCAACTAGTGGCAACATCTCGAAGGCTTGAGTTCACTTCTGAGCCCAAT 1953
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QY 1954 GAGTTCAGTCCGACAGCTTTCTAGCGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2013
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QY 2554 GCTGCTTTTGATCAGACTCTCTTAAGAGTGAAGTCAAGATCATCTCAGAGCAATTTGT 2613
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Db 2641 AAGCAGAGAGAAATGACAGATGCCCCCTCAGCTTGCTCATGTCAAACTGAATTA 2694
RESULT 7
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegen, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNO5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNO5-1
US-09-810-796-2
Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
QY 1 ATGAGAGATGAGTCCGAGCCGAGGAGGAGTCTGAACTGGGACCGCCGAGGAGC 60
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QY 1834 GACTATCAAGCCCTGATAGCAAGATCTTTCGGGTTCCGACAAAACAGTGCCTC 1893
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QY 1894 TTTATCAGATCAATGATGCAACATCTGAGAGGCTGCAAGTTCAATTGACGCCAAT 1953
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Db 2641 AAGGCAAGGAAAGTACAGATGCTTCAAGTGTCTCATGTCAAACTGAATAT 2694

RESULT 8
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1

GENERAL INFORMATION:
APPLICANT: DMOREZKY, STEVEN I
APPLICANT: RAMANATHAN, CHANDRA S
APPLICANT: TROJANACKI, JOANNE T
APPLICANT: ROISSARD, CHRISTOPHER G
APPLICANT: GRIKOFF, VALENTIN K
TITLE OF INVENTION: HUMAN KCNOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: D0023 DIV
CURRENT APPLICATION NUMBER: US/10/948,493
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: 60/207,389
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2694
TYPE: DNA
ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 98.6%; Score 2630; DB 21; Length 2694;

Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

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Db 121 AGGAGAGCGCGCGGCGGCGAGGAGGCGCGGATGAGCTGCTGGGAGAACGCTCTCT 180
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QY 1354 ACTGATGATGATATGATGAAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGATGATG 1413
Db 1381 ACTGATGATGATATGATGAAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGATGATG 1440
QY 1414 CCACCACTTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1473
Db 1441 CCACCACTTAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1474 AAGTTTAAGAAAGCTTACGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1533
Db 1501 AAGTTTAAGAAAGCTTACGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1534 GGTCACTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1593
Db 1561 GGTCACTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1594 GGAAGAGGCAATATCATCATGATGAAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1653
Db 1621 GGAAGAGGCAATATCATCATGATGAAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1680
QY 1654 ACCACAGAGATCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
Db 1681 ACCACAGAGATCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1714 ATAGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1773
Db 1741 ATAGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY 1774 GCCTAGGCCCTGCTTGGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT 1833

Db 1801 GCCTGAGCCCTCGCTTGGCTTATTCAGATCCACCTTTGTAATGTAAGAGACTCT 1860
Qy 1834 GACTATTAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCGCCACAACCACTGGCTGC 1893
Db 1861 GACTATTAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCGCCACAACCACTGGCTGC 1920
Qy 1894 TTATCCAGATCACTAGTGCACATCTCGAGAGAGCCCTGAGATTCACTTTCAGAGCCAAAT 1953
Db 1921 TTATCCAGATCACTAGTGCACATCTCGAGAGAGCCCTGAGATTCACTTTCAGAGCCAAAT 1980
Qy 1954 GAGTTCAGTCCCGCAGACTTTCTAGCGCTTACGCCCTAATAAGCAAGTCAAGCAACAG 2013
Db 1981 GAGTTCAGTCCCGCAGACTTTCTAGCGCTTACGCCCTAATAAGCAAGTCAAGCAACAG 2040
Qy 2014 GTGCCAATTTAGTCAAAAGCATGGTCTGACAGTGGCAGCCCAACACCATTTGCAACCA 2073
Db 2041 GTGCCAATTTAGTCAAAAGCATGGTCTGACAGTGGCAGCCCAACACCATTTGCAACCA 2100
Qy 2074 ATAAATACGGGACCCCAAGCCAGCCCAACCACTTACAGATCCCACTCCCTCCCA 2133
Db 2101 ATAAATACGGGACCCCAAGCCAGCCCAACCACTTACAGATCCCACTCCCTCCCA 2160
Qy 2134 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGCAACCTTAACCTGCAAGCTTACAGAA 2193
Db 2161 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGCAACCTTAACCTGCAAGCTTACAGAA 2220
Qy 2194 AGCATTTCTGACGTCAACACCTCTGTTGCTTCCCAAGAAATGTTCAAGTTGCAAG 2253
Db 2221 AGCATTTCTGACGTCAACACCTCTGTTGCTTCCCAAGAAATGTTCAAGTTGCAAG 2280
Qy 2254 TCAAAATCTCAAGGACCGCTTCTATGAGGAAAGCTTTCATGAGGAGGAGAACTCTG 2313
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Qy 2314 TTGTCTGTCTGTCCCATGTGTCGCAAGAACTTTCGCTGCTGCAAAACCTG 2373
Db 2341 TTGTCTGTCTGTCCCATGTGTCGCAAGAACTTTCGCTGCTGCAAAACCTG 2400
Qy 2374 ATCAAGTTCAGCCGAGAACTGAATATACAACTTTCAGGAGTGAATGCTCCAGA 2433
Db 2401 ATCAAGTTCAGCCGAGAACTGAATATACAACTTTCAGGAGTGAATGCTCCAGA 2460
Qy 2434 GGGAGCCAAAGATTTTACCCCAATGAGGAGAAATCCAAATTTGTTTAACTGAAGAG 2493
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Qy 2494 GTGGGTCCGAAAGAGACAGAGACACATTTTGTATGTCGCGACCGCAGCTGCAGGAA 2553
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Db 2581 GCTGCTTTTCATCAGACTCTCTTAAGAGCTGGAAGGTCAGATCATCTCAGACATTTGT 2640
Qy 2614 AAGGAGGAGAAAGTACAGATGCCCTCAGCTGCTCATATGCAAACTGAATAA 2667
Db 2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTGCTCATATGCAAACTGAATAA 2694

RESULT 9

US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US2002010267A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICGen, Inc.
; TITLE OF INVENTION: KCON5, a No. US2002010267A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS (2703)
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCON5-1
US-09-810-796-1

Query Match 98.5%; Score 2626.4; DB 9; Length 3071;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 ATGAAGATGTGAGTCCGGGCGGCGGAGGAGTCTGTAACCTCGACCCGAGGGGC 60
Db 10 ATGAAGATGTGAGTCCGGGCGGCGGAGGAGTCTGTAACCTCGACCCGAGGGGC 69
Qy 61 GACGCGCTGCTACTGCTGCGGCAACCGCGCGCCACGCTTGTGCGCGCGGCGTGCCTG 120
Db 70 GACGCGCTGCTACTGCTGCGGCAACCGCGCGCCACGCTTGTGCGCGCGGCGTGCCTG 129
Qy 121 AGGAGAGCGCGCGGCGGCAAGAGGCGCGCGGAGTGAAGCTGCGGAGAGCGCTCTCT 180
Db 130 AGGAGAGCGCGCGGCGGCAAGAGGCGCGCGGAGTGAAGCTGCGGAGAGCGCTCTCT 189
Qy 181 TACACAGATGAGCAGAGTCCGCGCGCAACGTCAGATACCGCGGAGTGAAGACTACCTG 240
Db 190 TACACAGATGAGCAGAGTCCGCGCGCAACGTCAGATACCGCGGAGTGAAGACTACCTG 249
Qy 241 TACACGCTGCTGAGAGACCCCGCGCGGCGGCTTCACTTCAACGCTTCTGTTTCTC 300
Db 250 TACACGCTGCTGAGAGACCCCGCGCGGCGGCTTCACTTCAACGCTTCTGTTTCTC 309
Qy 301 CTGTGCTTGTGCTGCTGATTTTTCAGGTTTTCAGATCCCGAGAGCAAAATG 360
Db 310 CTGTGCTTGTGCTGCTGATTTTTCAGGTTTTCAGATCCCGAGAGCAAAATG 369
Qy 361 GCTCAAGTTGCTCTGATTCCTGAGTTCGATGATGTCGCTTGTGTTGAGTTC 420
Db 370 GCTCAAGTTGCTCTGATTCCTGAGTTCGATGATGTCGCTTGTGTTGAGTTC 429
Qy 421 ATCAATGATCTGTGTCGCGGCTGCTGTTGATATAGAGATGCAAGAGACTG 480
Db 430 ATCAATGATCTGTGTCGCGGCTGCTGTTGATATAGAGATGCAAGAGAGACTG 489
Qy 481 AGTTTGTCTGAAAGCCCTTCTGTATAGATACCATTTGTTTCTTAATGAGCA 540
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Db 550 GTTGTTCGCAAAAACCTCAGGGTAATATTTTTCGACCTGCACTCAGAGTCTCCGT 609
Qy 601 TTCTTACAGATCCTCGCATGCTGTCGATGACCGAAGGGAGGCACTTGAATTAATCTG 660
Db 610 TTCTTACAGATCCTCGCATGCTGTCGATGACCGAAGGGAGGCACTTGAATTAATCTG 669
Qy 661 GGTTCAGTGTATGCTCAACAGAAATTAATACAGCTTGTGATCAATAGATTTTG 720
Db 670 GGTTCAGTGTATGCTCAACAGAAATTAATACAGCTTGTGATCAATAGATTTTG 729
Qy 721 GTTCTAATTTTTCGCTTCTTCTGCTATCTGTCGAAAGAGATCAATTAAGAGTTT 780
Db 730 GTTCTAATTTTTCGCTTCTTCTGCTATCTGTCGAAAGAGATCAATTAAGAGTTT 789
Qy 781 TCTACATATGAGATGCTCTGTGTGGGCAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 790 TCTACATATGAGATGCTCTGTGTGGGCAATTAATTAATTAATTAATTAATTAATTAAT 849

QY 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGACAGGCTTTGCACTCTTGGC 900
Db 850 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGACAGGCTTTGCACTCTTGGC 909
QY 901 ATTTCTTTCTTTGCACTTCTGCGGCACTTTGGCTCAGGTTTTCATTTAAAGTACA 960
Db 910 ATTTCTTTCTTTGCACTTCTGCGGCACTTTGGCTCAGGTTTTCATTTAAAGTACA 969
QY 961 GAACAACACCGCAGAAAACATTTGAGAAAAGAAAGAACCCAGCTCCCACTTCATTCAG 1020
Db 970 GAACAACACCGCAGAAAACATTTGAGAAAAGAAAGAACCCAGCTCCCACTTCATTCAG 1029
QY 1021 TGTGTTTGGCGTAACTTACGCACTGATGAGAAAATCTGTTTCCATTGCAACTTGAAGCA 1080
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QY 1081 CACTTGAAGGCTTTGACACCTGACGCTTACCA----- 1115
Db 1090 CACTTGAAGGCTTTGACACCTGACGCTTACCAAGAAAAGAACAGGGAAGCATCAAGC 1149
QY 1116 --TCAGAACTAAGTTTAAAGACGAGTGCATGAGTCCAGGAGGCGCAGATATT 1173
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QY 1294 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATAGTGTGACACAGCCCTTGGC 1353
Db 1330 TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGTATAGTGTGACACAGCCCTTGGC 1389
QY 1354 ACTGATGATGATATATGATGAAAAAGATGCAAGTGTGATCACTGAGAGACCTCAC 1413
Db 1390 ACTGATGATGATATATGATGAAAAAGATGCAAGTGTGATCACTGAGAGACCTCAC 1449
QY 1414 CCACCACTTAAACCTGCAATGAGCTATCAGAAATTATGAAATTTCAATGTCMAAAGG 1473
Db 1450 CCACCACTTAAACCTGCAATGAGCTATCAGAAATTATGAAATTTCAATGTCMAAAGG 1509
QY 1474 AAGTTTAAAGAAAAGTTACGTCCATATGATGTTAAAGATGTCATTGAACAATTTGCT 1533
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Db 1630 GGAAGAGGGCAATCATCAGATAGAAAGGCGAGAGAAAATTAACAGACAGCTAG 1689
QY 1654 ACCACAGAGATCTCAGTATGCTCGGTGCGGTGCTCAAGTTGAAAAAGAGTACAGTCC 1713
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QY 1714 ATAGAGTCCAGTGAAGTGCCTACTAGACATTTATCAACAGGTCTTTCGAAAGGCTCT 1773
Db 1750 ATAGAGTCCAGTGAAGTGCCTACTAGACATTTATCAACAGGTCTTTCGAAAGGCTCT 1809
QY 1774 GCCTCAGCCCTGCTTTGGCTTCAATCCAGATCCGCTTTGAATGTAAGACAGCATCT 1833
Db 1810 GCCTCAGCCCTGCTTTGGCTTCAATCCAGATCCGCTTTGAATGTAAGACAGCATCT 1869
QY 1834 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAAGTGGCTGC 1893
Db 1870 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGCAAAAAGTGGCTGC 1929

QY 1894 TTATCAGATCAACTAGTCCAAACATCTTCAGAGAGGCTTGCAGTTCAATCTGACGCCAAT 1953
Db 1930 TTATCAGATCAACTAGTCCAAACATCTTCAGAGAGGCTTGCAGTTCAATCTGACGCCAAT 1989
QY 1954 GAGTTCAGTCCCAACATTTCTAGCGGCTTACGCGCTTATGAGCAAGTCAAGCAACACAG 2013
Db 1990 GAGTTCAGTCCCAACATTTCTAGCGGCTTACGCGCTTATGAGCAAGTCAAGCAACACAG 2049
QY 2014 GTGCCAATTAGTCAAAAGGAGTGGCTCAGCAGTGGAGGCGACCAACCAATTGCAACCA 2073
Db 2050 GTGCCAATTAGTCAAAAGGAGTGGCTCAGCAGTGGAGGCGACCAACCAATTGCAACCA 2109
QY 2074 ATAAATACGGCACCCCAAGCAGAGCCCAACAACATTTACAGATCCACTCTCTCCA 2133
Db 2110 ATAAATACGGCACCCCAAGCAGAGCCCAACAACATTTACAGATCCACTCTCTCCA 2169
QY 2134 GCCATCAAGCATCTGCGCAGGCGAAGAACTGTGACCCCTTAACCCGTGAGGCTTACAGGA 2193
Db 2170 GCCATCAAGCATCTGCGCAGGCGAAGAACTGTGACCCCTTAACCCGTGAGGCTTACAGGA 2229
QY 2194 AGCATTTCTGACGTCACCACTGCTGTTGCTTCAAGAAAATGTTCAAGTTGACAG 2253
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QY 2254 TCAAAATCTCACCAAGACCGTTCTATGAGAAAAGCTTTGACATGAGAGAAAACCTGT 2313
Db 2290 TCAAAATCTCACCAAGACCGTTCTATGAGAAAAGCTTTGACATGAGAGAAAACCTGT 2349
QY 2314 TTGCTGTCTGTGCTGCTGATGTCGAGGAACTTTGGCAAAATCTTGTCTGTGCAAAACCTG 2373
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QY 2374 ATCAGGTGACCGAGAACTGAATATACACTTTTCAAGGAGTGAATCAAGTGCCTCAGA 2433
Db 2410 ATCAGGTGACCGAGAACTGAATATACACTTTTCAAGGAGTGAATCAAGTGCCTCAGA 2469
QY 2434 GGCAGCCAAAGATTTTACCACCAATGAGGAAATGCAAAATGTTTATTAATCATGATAAG 2493
Db 2470 GGCAGCCAAAGATTTTACCACCAATGAGGAAATGCAAAATGTTTATTAATCATGATAAG 2529
QY 2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGTATGTCGCGACCGCAGCGAGGA 2553
Db 2530 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGTATGTCGCGACCGCAGCGAGGA 2589
QY 2554 GCTGCTTTGATCAGACTCTCTTAAGACTGGAAGTCAAGATCTCAGAGCAATTTGT 2613
Db 2590 GCTGCTTTGATCAGACTCTCTTAAGACTGGAAGTCAAGATCTCAGAGCAATTTGT 2649
QY 2614 AAGCAGAGAAAAGTACAGATGCTTCAAGCTTGGCTCTCATGTCAAACTGAATTA 2667
Db 2650 AAGCAGAGAAAAGTACAGATGCTTCAAGCTTGGCTCTCATGTCAAACTGAATTA 2703

RESULT 10
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Query Match 98.4%; Score 2625.2; DB 19; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAGAGATGTGAGTGGGCGGGGAGGGTGTCTGTGAACCTCGAGCGCCGAGGGG 60
DB 1 ATGAGAGATGTGAGTGGGCGGGGAGGGTGTCTGTGAACCTCGAGCGCCGAGGGG 60
QY 61 GAGGGCGTGTACTGTCTGGGCAACCGGCGGCAAGCTTGTGGCGGCGGCGGCTG 120
DB 61 GAGGGCGTGTACTGTCTGGGCAACCGGCGGCAAGCTTGTGGCGGCGGCGGCTG 120
QY 121 AGGAGAGCGCGCGGGGCAAGAGGGGCGCGAGTGAAGCTGTGGGGAAGCGCTCT 180
DB 121 AGGAGAGCGCGCGGGGCAAGAGGGGCGCGAGTGAAGCTGTGGGGAAGCGCTCT 180
QY 181 TACACGAGTAGCCAGAGCTCCCGCGCAAGTCAAGTCCGCGGAGTGCAAACTAC 240
DB 181 TACACGAGTAGCCAGAGCTCCCGCGCAAGTCAAGTCCGCGGAGTGCAAACTAC 240
QY 241 TACAGCGTGTGAGAGACCCCGCGGCTGTCACTCAACCGCTTCTGTTTTCTC 300
DB 241 TACAGCGTGTGAGAGACCCCGCGGCTGTCACTCAACCGCTTCTGTTTTCTC 300
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DB 361 GCCTCAAGTTGCCCTTTGATCTGTGAGTTCGTGATGTTGCTTTGGTTGAGTT 420
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DB 841 GACAAACTCCCTTAACTTGGCTGTGGAAATGCTTCTGAGGCTTTGCACTCT 900
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DB 1081 CACTTGAAGCCTTGGACACCTGACGCTTACCA----- 1115
QY 1116 --TCAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCGGAGTAT 1173
DB 1116 --TCAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCGGAGTAT 1173
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DB 1294 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACAGCCCTTGGC 1353
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DB 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATGCTGACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
DB 1354 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
QY 1381 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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DB 1414 CCAACCTTAAACCTGTCACTTGAAGTATCAAGATTTATGAAATTTATGTTGCAAA 1473
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DB 1441 CCAACCTTAAACCTGTCACTTGAAGTATCAAGATTTATGAAATTTATGTTGCAAA 1500
QY 1474 AAGTTTAAAGAAACGTTAGTCAATGATGATGATGATGATGATGATGATGATGAT 1533
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QY 1594 GGAAGAGGCGAAATCATCATGATTAAGAGAGCGGAGAAATTAACAGAGAACTGAG 1653
DB 1594 GGAAGAGGCGAAATCATCATGATTAAGAGAGCGGAGAAATTAACAGAGAACTGAG 1653
QY 1621 GGAAGAGGCGAAATCATCATGATTAAGAGAGCGGAGAAATTAACAGAGAACTGAG 1680
DB 1621 GGAAGAGGCGAAATCATCATGATTAAGAGAGCGGAGAAATTAACAGAGAACTGAG 1680
QY 1654 ACCAGAGATCTCATGATGCTCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1713
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QY 1681 ACCAGAGATCTCATGATGCTCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
DB 1681 ACCAGAGATCTCATGATGCTCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
QY 1714 ATGAGTCCAGCTGAGTCTGCTACTAGACATCTATCAACAGGTCCTTGGAAAGCTCT 1773
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QY 1834 GACTATCAAGGCTGTGATGCAAGATCTTGTGGGTTCCGACAAAGAGTGGCTGC 1893
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DB 1861 GACTATCAAGGCTGTGATGCAAGATCTTGTGGGTTCCGACAAAGAGTGGCTGC 1920
QY 1894 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAGTTCATTTGACGCCAAAT 1953
DB 1894 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAGTTCATTTGACGCCAAAT 1953
QY 1921 TTATCCAGATCAATAGTCCCAACATCTGAGAGGCTGCAGTTCATTTGACGCCAAAT 1980
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QY 1954 GAGTTAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTACTATGACAGTCAACACAG 2013
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QY 1981 GAGTTAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTACTATGACAGTCAACACAG 2040
DB 1981 GAGTTAGTCCCAAGCTTTCTACGCGCTTACGCTTACCTACTATGACAGTCAACACAG 2040
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DB 2041 GTGCCAATTATGTCAAAGGATGCTCAGAGTGGGAGCCCAACCAACATTTGCAACCA 2100
QY 2074 ATTAATACGCAACCAAGCAAGCCCAACCAACATTTACAGATCCACCTCTCCCA 2133
DB 2074 ATTAATACGCAACCAAGCAAGCCCAACCAACATTTACAGATCCACCTCTCCCA 2133

Db 2101 ATAAATACGACCCAGGACGAGCCCAACAACTTTACAGATCCACCTCTCCCA 2160
Qy 2134 GCATATAGCATGTGCCAGGACGAGAACTCTGCAACCTTAACCTTCAGGCTTACAGAA 2193
Db 2161 GCATATAGCATGTGCCAGGACGAGAACTCTGCAACCTTAACCTTCAGGCTTACAGAA 2220
Qy 2194 AGCATTTCTGACGTCAACAACCTGCTTGTGCTCCAGAGAAATGTTGAGGTGACAG 2253
Db 2221 AGCATTTCTGACGTCAACAACCTGCTTGTGCTCCAGAGAAATGTTGAGGTGACAG 2280
Qy 2254 TCAATCTCAACCAAGAACGCTTATAGAGAAAGCTTTGACATGGAGAGAAATCTCG 2313
Db 2281 TCAATCTCAACCAAGAACGCTTATAGAGAAAGCTTTGACATGGAGAGAAATCTCG 2340
Qy 2314 TTGTCTGTCTGTCCTCCAGTGGCGAGAGACTTGGGCAAACTTTGTCTGCAAAACCTG 2373
Db 2341 TTGTCTGTCTGTCCTCCAGTGGCGAGAGACTTGGGCAAACTTTGTCTGCAAAACCTG 2400
Qy 2374 ATCAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCAGA 2433
Db 2401 ATCAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCAGA 2460
Qy 2434 GGCAGCCAGATTTTATACCCCAATGGAGGAATCCAAATGTTTATCTGATGAAG 2493
Db 2461 GGCAGCCAGATTTTATACCCCAATGGAGGAATCCAAATGTTTATCTGATGAAG 2520
Qy 2494 GTGGGTCCGGAAGAGACAGACACACTTTGATGCGCACCGAGCTGCGAGAGAA 2553
Db 2521 GTGGGTCCGGAAGAGACAGACACACTTTGATGCGCACCGAGCTGCGAGAGAA 2580
Qy 2554 GCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGATCATCTGAGCAATTTGT 2613
Db 2581 GCTGCTTTGATCAGACTCTCTAAGAGCTGGAAGTCAAGATCATCTGAGCAATTTGT 2640
Qy 2614 AAGGCAAGAGAAAGTACAGATGCTTCAAGTGGCTTCAATGTAATAA 2667
Db 2641 AAGGCAAGAGAAAGTACAGATGCTTCAAGTGGCTTCAATGTAATAA 2694

RESULT 11

US-09-813-148-1

/ Sequence 1, Application US/09813148
/ Patent No. US20020076809A1
/ GENERAL INFORMATION:
/ APPLICANT: STEINMEYER, Klaus
/ APPLICANT: LERCHE, Christian
/ APPLICANT: SCHERER, Constanze
/ APPLICANT: SEEBOM, Guiscard
/ APPLICANT: BUSCH, Andreas E.
/ TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
/ FILE REFERENCE: 38005-119
/ CURRENT APPLICATION NUMBER: US/09/813,148
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: DE 100 13 732.6
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/194,041
/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 98.1%; Score 2617.2; DB 9; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

Qy 1 ATGAAGATGTGAGACTCGGCGCGGAGGCTGCTGAACTCGGACCGCCAGGGGC 60
|||||

Db 215 ATGAAGATGTGAGACTCGGCGCGGAGGCTGCTGAACTCGGACCGCCAGGGGC 274
Qy 61 GACGCGCTGTACTCTGTGGGACCCCGCGGACAGCTTGTGTGGCGGCGGCTGCTG 120
Db 275 GACGCGCTGTACTCTGTGGGACCCCGCGGACAGCTTGTGTGGCGGCGGCTGCTG 334
Qy 121 AAGGAGACCGCGGAGCAAGGAGGAGCCCGGATGAGCTTGTGGGAAAGCGCTCTCT 180
Db 335 AAGGAGACCGCGGAGCAAGGAGGAGCCCGGATGAGCTTGTGGGAAAGCGCTCTCT 394
Qy 181 TACAGATGTGAGAGAGTGGCGGCGCAACGTCAAGTACCGCGGCTGACAACTACCTG 240
Db 395 TACAGATGTGAGAGAGTGGCGGCGCAACGTCAAGTACCGCGGCTGACAACTACCTG 454
Qy 241 TACAAGTGTGAGAGAGACCCCGCGGCTGAGGCTCATCTACAGCTTGTGTTTTCTC 300
Db 455 TACAAGTGTGAGAGAGACCCCGCGGCTGAGGCTCATCTACAGCTTGTGTTTTCTC 514
Qy 301 CTTGTCTTTGGTGTGATTTTGTCAAGTTTTTCTACATTCCTGAGCACAAATTTG 360
Db 515 CTTGTCTTTGGTGTGATTTTGTCAAGTTTTTCTACATTCCTGAGCACAAATTTG 574
Qy 361 GCGTCAAGTGGCTCTTGAATCTCGAGTTCGTGAATTTGTGCTTGTGGAGTTC 420
Db 575 GCGTCAAGTGGCTCTTGAATCTCGAGTTCGTGAATTTGTGCTTGTGGAGTTC 634
Qy 421 ATCATTCGAATCTGTGCTCGGAGTGTCTGTGCTGATTAAGAGATGCAAGAAAGACTG 480
Db 635 ATCATTCGAATCTGTGCTCGGAGTGTCTGTGCTGATTAAGAGATGCAAGAAAGACTG 694
Qy 481 AAGTTGCTCGAAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 540
Db 695 AAGTTGCTCGAAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATGCTTCAATAGCA 754
Qy 541 GTTGTCTGCAAAAACCTCAGGTAATTTTGTGCACTGCTGCACTGAGAAGTCCGT 600
Db 755 GTTGTCTGCAAAAACCTCAGGTAATTTTGTGCACTGCTGCACTGAGAAGTCCGT 814
Qy 601 TTCTACAGATCTCTCCGATGATGCGAGTGAACCGAAGGAGGACCTTGAATTAATCTG 660
Db 815 TTCTACAGATCTCTCCGATGATGCGAGTGAACCGAAGGAGGACCTTGAATTAATCTG 874
Qy 661 GGTTCAGTGTATTATGCTCAACAGCAAGAAATTAATCAAGCTTGTGATAGATTTTGTG 720
Db 875 GGTTCAGTGTATTATGCTCAACAGCAAGAAATTAATCAAGCTTGTGATAGATTTTGTG 934
Qy 721 GTTCTTATTTTGTGCTTCTTCTGCTATCTGAGTGAAGAAAGATGCCAATTAAGATTT 780
Db 935 GTTCTTATTTTGTGCTTCTTCTGCTATCTGAGTGAAGAAAGATGCCAATTAAGATTT 994
Qy 781 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATGACATTAATGCTATGGA 840
Db 995 TCTACATATGAGATGCTCTGTGTGGGCACAATTAATGACATTAATGCTATGGA 1054
Qy 841 GACAAAATCTCCCTTAACCTTGTGAGAAAGATTTGTTTGTGACAGCTTGTGCACTCTTGGC 900
Db 1055 GACAAAATCTCCCTTAACCTTGTGAGAAAGATTTGTTTGTGACAGCTTGTGCACTCTTGGC 1114
Qy 901 ATTTCTTCTTTGACCTTCTGCGGCACTTCTGAGTGAAGTTTGTGATTAAGATACAA 960
Db 1115 ATTTCTTCTTTGACCTTCTGCGGCACTTCTGAGTGAAGTTTGTGATTAAGATACAA 1174
Qy 961 GAACAACCGCGCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTTACG 1020
Db 1175 GAACAACCGCGCAGAAAACCTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTTACG 1234
Qy 1021 TGTGTTTGGGTAGTTACGACGCTGATGAGAAATCTGTTTCAATTGCAACTGGAAGCCA 1080
Db 1235 TGTGTTTGGGTAGTTACGACGCTGATGAGAAATCTGTTTCAATTGCAACTGGAAGCCA 1294
Qy 1081 CACTTGAAGGCTTGGACACCTGACAGCTTACCA----- 1115
Db 1295 CACTTGAAGGCTTGGACACCTGACAGCTTACCA----- 1354

QY 1116 --TCAGAGCTAAGTTTAAAGAGCGAGTGGCTAGGCCCAAGGGCCAGAGATT 1173
 DB 1355 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCTAGGCCCAAGGGCCAGAGATT 1414
 QY 1174 AAGAGCCGACAGGCTCAGTATGAGGAGAGTCCCAAGCAACGACATCAGAGCCGAG 1233
 DB 1415 AAGAGCCGACAGGCTCAGTATGAGGAGAGTCCCAAGCAACGACATCAGAGCCGAG 1474
 QY 1234 GGCAGTCCCAAGAGTGAAGAGTGGAGCTTCAAGACCGAGCCGCTCCGCGCC 1293
 DB 1475 GGCAGTCCCAAGAGTGAAGAGTGGAGCTTCAAGACCGAGCCGCTCCGCGCC 1534
 QY 1294 TCGCTGCGCTCAAAAGTTCTCAGCCCAACAGTGTATAGTCTGACACAGCCTTGGC 1353
 DB 1535 TCGCTGCGCTCAAAAGTTCTCAGCCCAACAGTGTATAGTCTGACACAGCCTTGGC 1594
 QY 1354 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTATATCAGTGAAAGCTTACC 1413
 DB 1595 ACTGATGATGTATATGATGAAAAAGATGCGCAGTGTATATCAGTGAAAGCTTACC 1654
 QY 1414 CCACCACTTAAACCTGCTATGAGCTATCAGAAATTAAGAAATTTGATGTAACCG 1473
 DB 1655 CCACCACTTAAACCTGCTATGAGCTATCAGAAATTAAGAAATTTGATGTAACCG 1714
 QY 1474 AAGTTTAAAGAAAGTTACGTCATATGATGTAAGATGTCATTTGAACAAATTTCTGCT 1533
 DB 1715 AAGTTTAAAGAAAGTTACGTCATATGATGTAAGATGTCATTTGAACAAATTTCTGCT 1774
 QY 1534 GGTCTATGCGACATGTTGTGTAGAAATTAAGAGCTTTCAACAGGTGTATCAAAATTTCT 1593
 DB 1775 GGTCTATGCGACATGTTGTGTAGAAATTAAGAGCTTTCAACAGGTGTATCAAAATTTCT 1834
 QY 1594 GGAAAGGGGCAATTCATCAGATTAAGAAAGCGGAGAAATTAACAGAGAACTGAG 1653
 DB 1835 GGAAAGGGGCAATTCATCAGATTAAGAAAGCGGAGAAATTAACAGAGAACTGAG 1894
 QY 1654 ACCACAGAGATCTCAGTATGCTCGGTGGGTGCTCAAGGTGTAAGAAACAGTACGCTC 1713
 DB 1895 ACCACAGAGATCTCAGTATGCTCGGTGGGTGCTCAAGGTGTAAGAAACAGTACGCTC 1954
 QY 1714 ATAGAGTCCAGGTGAGTGGCTTACATGATCAATCAACAGGTCTCTCGAAAGGCTCT 1773
 DB 1955 ATAGAGTCCAGGTGAGTGGCTTACATGATCAATCAACAGGTCTCTCGAAAGGCTCT 2014
 QY 1774 GCTCAGCCCTCGCTTGGCTTATTCAGATCCCACTTTTGAATGTGAACAGATCT 1833
 DB 2015 GCTCAGCCCTCGCTTGGCTTATTCAGATCCCACTTTTGAATGTGAACAGATCT 2074
 QY 1834 GACTATCAAGGCTGTGATAGCAAGATCTTTGCGGTTCCGCAAAAAGTGGCTGC 1893
 DB 2075 GACTATCAAGGCTGTGATAGCAAGATCTTTGCGGTTCCGCAAAAAGTGGCTGC 2134
 QY 1894 TTATCCAGATCAATAGTGGCAACATCTCGAGAGGCTTCAAGTTCTGAGCCCAAT 1953
 DB 2135 TTATCCAGATCAATAGTGGCAACATCTCGAGAGGCTTCAAGTTCTGAGCCCAAT 2194
 QY 1954 GAGTTCAAGTCCCAAGCTTTTCTAGCGGCTTACGCTTACATAGCAAGTCAAGCAACAG 2013
 DB 2195 GAGTTCAAGTCCCAAGCTTTTCTAGCGGCTTACGCTTACATAGCAAGTCAAGCAACAG 2254
 QY 2014 GTGCCCAATTAAGTCAAGGATGGCTCAGAGTGGAGCCCAACCAACATTTGCAACCA 2073
 DB 2255 GTGCCCAATTAAGTCAAGGATGGCTCAGAGTGGAGCCCAACCAACATTTGCAACCA 2314
 QY 2074 ATTAATTAAGGCAACCAAGCCAGGCAACCAACATTTTCAAGTCCACCTCTCTCCA 2133
 DB 2315 ATTAATTAAGGCAACCAAGCCAGGCAACCAACATTTTCAAGTCCACCTCTCTCCA 2374
 QY 2134 GGCATCAAGCATCTGCGCAGGCGCAAGAAATCTGCAACCTTACAGAGAA 2193
 DB 2375 GGCATCAAGCATCTGCGCAGGCGCAAGAAATCTGCAACCTTACAGAGAA 2434

QY 2194 AGCATTTCTAGCTACCAACCTGCTTGTGCTCCAGAAATTTGATGAGTGCAG 2253
 DB 2435 AGCATTTCTAGCTACCAACCTGCTTGTGCTCCAGAAATTTGATGAGTGCAG 2494
 QY 2254 TCAATCTCAACCAAGGACCGTTCTATGAGAAAAAGTTTGAATGAGAGAACTCTG 2313
 DB 2495 TCAATCTCAACCAAGGACCGTTCTATGAGAAAAAGTTTGAATGAGAGAACTCTG 2554
 QY 2314 TTGTCTGTCTGCTCCATGAGTGGCGAAGGACTTGGGCAATCTTTGTCTGCAAACTG 2373
 DB 2555 TTGTCTGTCTGCTCCATGAGTGGCGAAGGACTTGGGCAATCTTTGTCTGCAAACTG 2614
 QY 2374 ATCAGGTCCAGGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCAGA 2433
 DB 2615 ATCAGGTCCAGGAGAACTGAATATCAACTTTCAAGGAGTGAAGTCAAGTGGCTCAGA 2674
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 DB 2675 GGCAGCCAAAGTTTATCCCAATGAGAGGAAATCCAAATGTTTATTAATCTAGTAAAG 2734
 QY 2494 GTGGGTCCGGAAGACAGAGACAGACACTTTTGAATGCGCAGCCGAGCTCCAGAGAA 2553
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 QY 2554 GGTGCTTTGATCACTCTCTAAGACTGGAAGTCAAGATCTCAGAGCATTTGT 2613
 DB 2795 GGTGCTTTGATCACTCTCTAAGACTGGAAGTCAAGATCTCAGAGCATTTGT 2854
 QY 2614 AAGCAGAGAAAGTACAGATGCTTCAAGCTTGTCTCATGTCAAACTGAATTA 2667
 DB 2855 AAGCAGAGAAAGTACAGATGCTTCAAGCTTGTCTCATGTCAAACTGAATTA 2908

RESULT 12
 US-10-399-489A-5
 ; Sequence 5, Application US/10399489A
 ; Publication No. US20050101004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: ARGENTIERI, Thomas M.
 ; APPLICANT: SHELDON, Jeffrey H.
 ; TITLE OF INVENTION: METHODS OF SELECTING COMPOUNDS FOR MODULATION OF BLADDER FUNCTION
 ; FILE REFERENCE: AML06620
 ; CURRENT APPLICATION NUMBER: US/10/399,489A
 ; CURRENT FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: 60/241,078
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: PCT/US01/32371
 ; PRIOR FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 60/281,428
 ; PRIOR FILING DATE: 2001-04-04
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patencin version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-399-489A-5

Query Match 98.1%; Score 2617.2; DB 21; Length 3074;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;
 QY 1 ATGAAGATGTGAGTCCGCGCGGCGAGGCTGTGCTGAACTCGGACGCGCCAGGGG 60
 DB 215 ATGAAGATGTGAGTCCGCGCGGCGAGGCTGTGCTGAACTCGGACGCGCCAGGGG 274
 QY 61 GACGCGCTGTCTCTGCTGGGACCGCGCGGCGACGCTTGTGAGGCGGCGGCGGCGCTG 120
 DB 275 GACGCGCTGTCTCTGCTGGGACCGCGCGGCGACGCTTGTGAGGCGGCGGCGGCGCTG 334
 QY 121 AGGAGAGCGCGCGGCGGCGAGCAGGAGGCGCGGATGAGCTGTGAGGAGGCGCTCTT 180

335 AGGAGAGCGCCGCGGAGCAAGCAGGGGACCCGAGTAGCCTGTGGAAGCCGCTCTCT 394
181 TACACAGTAGGCAGAGCTGCGGCGCAAGTCAATGACCGGCGGATGCAAGTACTACTG 240
395 TACACAGTAGGCAGAGCTGCGGCGCAAGTCAATGACCGGCGGATGCAAGTACTACTG 454
241 TACAAAGTGTGAGAGAGACCCGCGGCTGCGGCTTCAATGACCAAGCTTTGTTTTCTC 300
455 TACAAAGTGTGAGAGAGACCCGCGGCTGCGGCTTCAATGACCAAGCTTTGTTTTCTC 514
301 CTTGCTTTGTTGTTGCTTGAATTTTGTCAAGTCTTTTCAACATCCCTGAGACCAAAATG 360
515 CTGTCTTTGTTGTTGCTTGAATTTTGTCAAGTCTTTTCAACATCCCTGAGACCAAAATG 574
361 GCCTCAAGTTGCTCTTGAATCTGAGATTGATGATTTGCTGCTTTGTTGAGTTTC 420
575 GCCTCAAGTTGCTCTTGAATCTGAGATTGATGATTTGCTGCTTTGTTGAGTTTC 634
421 ATCAATTCGAATCTGTGCTGCGGCTGCTGTTGTCGATATAGAGATGCAAGAGACTG 480
635 ATCAATTCGAATCTGTGCTGCGGCTGCTGTTGTCGATATAGAGATGCAAGAGACTG 694
481 AGGTTTGCCTGAAAGCCCTTGTGTATAGATACCAATGTTCTTATGCTTCAATAGCA 540
695 AGGTTTGCCTGAAAGCCCTTGTGTATAGATACCAATGTTCTTATGCTTCAATAGCA 754
541 GTTGTCTTGCAGAAAACCTCAGGGTAAATATTTTTCACAGCTTGCACTCAGAAATCTCG 600
755 GTTGTCTTGCAGAAAACCTCAGGGTAAATATTTTTCACAGCTTGCACTCAGAAATCTCG 814
601 TTCTTACAGATCTCTCGCATGTGTGCGCATGAGACCGAAGGGAGGCACTTGGAAATTAATG 660
815 TTCTTACAGATCTCTCGCATGTGTGCGCATGAGACCGAAGGGAGGCACTTGGAAATTAATG 874
661 GGTTCAGTGGTTTATGCTCAGACAGAGAAATTAATCAGAGCTTGTATCATTAGATTTTGG 720
875 GGTTCAGTGGTTTATGCTCAGACAGAGAAATTAATCAGAGCTTGTATCATTAGATTTTGG 934
721 GTTCTTAATTTTTCGTCTTCTTCTTGTCTATCTGTGTGAAAAGAGATCCAAATAAGAGTT 780
935 GTTCTTAATTTTTCGTCTTCTTCTTGTCTATCTGTGTGAAAAGAGATCCAAATAAGAGTT 994
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995 TCTACATATGAGAGATGCTCTGTGTGGGCACAATTAATGACCAATTAATGAGTATGGA 1054
841 GACAAAACCTCCCTAATCTGTGGCTGGGAAAGATGCTTTGCAAGGCTTTCACCTCTGGC 900
1055 GACAAAACCTCCCTAATCTGTGGCTGGGAAAGATGCTTTGCAAGGCTTTCACCTCTGGC 1114
901 AATTTCTTCTTTCGACATCTCTGCGGCATTTCTTGCTCAGATTTTTCATTTAAAGTACA 960
1115 AATTTCTTCTTTCGACATCTCTGCGGCATTTCTTGCTCAGATTTTTCATTTAAAGTACA 1174
961 GAAACAACCCGCGCAAAACATTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTTGAG 1020
1175 GAAACAACCCGCGCAAAACATTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTTGAG 1234
1021 TGTGTTTGGGATAGTATGAGAGCTGATGAGAAATCTGTTTCAATTGCAACTTGGAGGCA 1080
1235 TGTGTTTGGGATAGTATGAGAGCTGATGAGAAATCTGTTTCAATTGCAACTTGGAGGCA 1294
1081 CACTTGAAGGCTTTCGACACTGACAGCCCTTACCA----- 1115
1295 CACTTGAAGGCTTTCGACACTGACAGCCCTTACCAAGAAAGAACAGAGGAGATCAAGC 1354
1116 --TCAGAGCTAAGTTTAAAGAGCAAGTGCATGAGCTTACCCAGGGGCCAGATATT 1173
1355 AGTCAAGAGCTAAGTTTAAAGAGCAAGTGCATGAGCTTACCCAGGGGCCAGATATT 1414
1174 AAGAGCGCAAGAGCTCAGTATGAGAGAGTCCCAAGAGCCGACCAATCAAGCGGAG 1233
1415 AAGAGCGCAAGAGCTCAGTATGAGAGAGTCCCAAGAGCCGACCAATCAAGCGGAG 1474

1234 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGCCC 1293
1475 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGCCC 1534
1294 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGATATGATGCTGACACAGCCCTTGGC 1353
1535 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGATATGATGCTGACACAGCCCTTGGC 1594
1354 ACTGATGATGATATGATGAGAAAAGAGATGCCAGTGTGATGATCAGTGAAGACCTCAC 1413
1595 ACTGATGATGATATGATGAGAAAAGAGATGCCAGTGTGATGATGATGATGAGACCTCAC 1654
1414 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAATGAAATTTTCAATGTCAAAACGG 1473
1655 CCACCACTTAAACCTGTCATTCGAGCTATCAGAAATTAATGAAATTTTCAATGTCAAAACGG 1714
1474 AAGTTAAGAGAAACCTTACGTCCTATGATGATGATGATGATGATGATGATGATGATGATG 1533
1715 AAGTTAAGAGAAACCTTACGTCCTATGATGATGATGATGATGATGATGATGATGATGATG 1774
1534 GGTCACTGAGACATGTTGTGATGAAATTAAGACCTTCAACACGTTGATCAAAATTCCT 1593
1775 GGTCACTGAGACATGTTGTGATGAAATTAAGACCTTCAACACGTTGATCAAAATTCCT 1834
1594 GGAAGAGGCAAAATCAGATCAGATTAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1653
1835 GGAAGAGGCAAAATCAGATCAGATTAAGAGCCGAGAGAAATTAACAGCAGACATGAG 1894
1654 ACCACAGACATCTCAGATATGCTGCTGCGGTGCTCAAGTTGAAACAGGTACAGTCC 1713
1895 ACCACAGACATCTCAGATATGCTGCTGCGGTGCTCAAGTTGAAACAGGTACAGTCC 1954
1714 ATAGAGTCCAAGCTGAGCTGCTTACTAGACATCTTCAACAGGTCTTCCGAAAAGCTCT 1773
1955 ATAGAGTCCAAGCTGAGCTGCTTACTAGACATCTTCAACAGGTCTTCCGAAAAGCTCT 2014
1774 GCTCAGCCCTGCTTGTGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT 1833
2015 GCTCAGCCCTGCTTGTGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT 2074
1834 GACTATCAAAAGCCCTGTGATGATGAGAAAGATCTTTGCGGTCCGCAAAACAGTGGCTG 1893
2075 GACTATCAAAAGCCCTGTGATGATGAGAAAGATCTTTGCGGTCCGCAAAACAGTGGCTG 2134
1894 TTATCCAGATCAACTAGTGCACCAATCTCGAAGAGCTGCAATTAATCTGACGCAAT 1953
2135 TTATCCAGATCAACTAGTGCACCAATCTCGAAGAGCTGCAATTAATCTGACGCAAT 2194
1954 GAGTTCAGTGCAGACATTTCTACGCGCTTACGCTTACCTTATGACAGTCAACAGACAG 2013
2195 GAGTTCAGTGCAGACATTTCTACGCGCTTACGCTTACCTTATGACAGTCAACAGACAG 2254
2014 GTGCCAATTAATGCAAAAGGATGCTCAGCAGTGGAGGACCAACACCAATTTGCAAAACCA 2073
2255 GTGCCAATTAATGCAAAAGGATGCTCAGCAGTGGAGGACCAACACCAATTTGCAAAACCA 2314
2074 ATAAATAGGCGCACCCAGACAGACAGCCCAACCACTTTACAGATCCACTCTCTCCA 2133
2315 ATAAATAGGCGCACCCAGACAGACAGCCCAACCACTTTACAGATCCACTCTCTCCA 2374
2134 GGCATCAAGCATCTGCGCAGGCAAGAACTGCAACCTTAACCTGCAAGGCTTACAGGAA 2193
2375 GGCATCAAGCATCTGCGCAGGCAAGAACTGCAACCTTAACCTGCAAGGCTTACAGGAA 2434
2194 AGCATTTTCAGAGTCAACCACTGCTTGTGTGCTTCAAGGAAATGTTCAAGGTTCACAG 2253
2435 AGCATTTTCAGAGTCAACCACTGCTTGTGTGCTTCAAGGAAATGTTCAAGGTTCACAG 2494
2254 TCAAAATCAACCAAGACCGTTCTATGAGAAAACCTTTGACATGAGAGAGAAAACCTGT 2313
2495 TCAAAATCAACCAAGACCGTTCTATGAGAAAACCTTTGACATGAGAGAGAAAACCTGT 2554

QY 2314 TTGCTGTCTGTCCTCCATGTCGCGAAGAGACTTGGCGCAATCTTGTGTGCAAAAACCTG 2373
Db 2555 TTGTCTGTCTGTCCCATGTCGCGAAGAGACTTGGCGCAATCTTGTGTGCAAAAACCTG 2614
QY 2374 ATCAGGTGCAACCGAAGACTGAAATATACAACTTTGAGGAGTGAAGTCAAGTGTGCTCCAGA 2433
Db 2615 ATCAGGTGCAACCGAAGACTGAAATATACAACTTTGAGGAGTGAAGTCAAGTGTGCTCCAGA 2674
QY 2434 GGCAGCCAAATTTTAAACCCCAATGAGGGAATCCAAATGTTTAACTGATGAAAGAG 2493
Db 2675 GGCAGCCAAATTTTAAACCCCAATGAGGGAATCCAAATGTTTAACTGATGAAAGAG 2734
QY 2494 GTGGGTCCCGAAGAGACAGAGACACACTTTTGTATGTCGCGACCGAGCTGCGAGGAA 2553
Db 2735 GTGGGTCCCGAAGAGACAGAGACACACTTTTGTATGTCGCGACCGAGCTGCGAGGAA 2794
QY 2554 GCTGCTTTTGCAATCAGACTCTCTTAAGAGCTGAAAGTCAAGTCAATCTCAGAGCAATTTGT 2613
Db 2795 GCTGCTTTTGCAATCAGACTCTCTTAAGAGCTGAAAGTCAAGTCAATCTCAGAGCAATTTGT 2854
QY 2614 AAGCGAGGAAGATACAGATGCGCTCAGCTTGCCTCATGTCAACTGAATAA 2667
Db 2855 AAGCGAGGAAGATACAGATGCGCTCAGCTTGCCTCATGTCAACTGAATAA 2908

RESULT 13

US-10-482-834A-55
Sequence 55, Application US/10482834A
Publication No. US20050074764A1
GENERAL INFORMATION:
APPLICANT: Mulley, John Charles
APPLICANT: Harlin, Louise Anne
APPLICANT: Dibiens, Michelle
APPLICANT: Wallace, Robyn
APPLICANT: Phillips, Hillary Amy
APPLICANT: Heron, Sara Elizabeth
APPLICANT: Berkovic, Samuel Frank
APPLICANT: Scheffer, Ingrid Eileen
APPLICANT: Biomedica Limited
TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
FILE REFERENCE: 1386/17
CURRENT APPLICATION NUMBER: US/10/482,834A
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-10-482-834A-55

Query Match 98.1%; Score 2615.6; DB 21; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2658; Conservative 0; Mismatches 9; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGAGTCCGGGCGGAGGAGGTCTGCTGAATCGGACGCGCAGAGGAG 60
Db 215 ATGAAGATGTGAGTCCGGGCGGAGGAGGTCTGCTGAATCGGACGCGCAGAGGAG 274
QY 61 GACGGCTCTACTGCTGAGGACCCGCGCGCCAGCCTGTGTGCGCGCGGCTGAGCTG 120
Db 275 GACGGCTCTACTGCTGAGGACCCGCGCGCCAGCCTGTGTGCGCGCGGCTGAGCTG 334
QY 121 AAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 335 AAGGAGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 394
QY 181 TACACAGTAGCAGAGAGCTGCGGCGCAACGTCAGAGTACCGGCGGAGTGAAGTCTACTG 240
Db 395 TACACAGTAGCAGAGAGCTGCGGCGCAACGTCAGAGTACCGGCGGAGTGAAGTCTACTG 454
QY 241 TACACAGTAGCAGAGAGCTGCGGCGCAACGTCAGAGTACCGGCGGAGTGAAGTCTACTG 300

Db 455 TACACAGTAGCAG 514
QY 301 CTGTGCTTTGGTGTGCTGATTTTGTGAGGTCTTTTCAACATCCCTAGAGACACAAATTTG 360
Db 515 CTGTGCTTTGGTGTGCTGATTTTGTGAGGTCTTTTCAACATCCCTAGAGACACAAATTTG 574
QY 361 GCCTCAAGTTGCTCTTGAATCCCTGAGTCTGAGTATGATTTGTGCTCTTTGGTTGAGTTTC 420
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QY 421 ATCATTGCAATCTGTCTGCGGAGTCTGTGTGATATAGAGATGAGAGAGAGAGAGAGAGAG 480
Db 635 ATCATTGCAATCTGTCTGCGGAGTCTGTGTGATATAGAGATGAGAGAGAGAGAGAGAGAG 694
QY 481 AGTTTGTGTCGAAGAGCCCTTGTGTATATAGATACATTTGTTTATGCTTCAATAGCA 540
Db 695 AGTTTGTGTCGAAGAGCCCTTGTGTATATAGATACATTTGTTTATGCTTCAATAGCA 754
QY 541 GTTGTGTTTGCAGAAAAGTCAAGGATATATTTTGTGCAAGTCTGCACTCAGAAAGTCCGCT 600
Db 755 GTTGTGTTTGCAGAAAAGTCAAGGATATATTTTGTGCAAGTCTGCAAGTCTCAGAAAGTCCGCT 814
QY 601 TTCTTACAGATCTCCGATGTGTGCGATGACCGAAGGAGAGAGCACTTGAATAATTACTG 660
Db 815 TTCTTACAGATCTCCGATGTGTGCGATGACCGAAGGAGAGAGCACTTGAATAATTACTG 874
QY 661 GGTTCAGTGTGTTATGCTCAACAGAGAAATTAATACAGCTTTGTGATATAGATTTTGTG 720
Db 875 GGTTCAGTGTGTTATGCTCAACAGAGAAATTAATACAGCTTTGTGATATAGATTTTGTG 934
QY 721 GTTCTTATTTTTCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 935 GTTCTTATTTTTCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
QY 781 TCTACATATGAGATGCTCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 995 TCTACATATGAGATGCTCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1054
QY 841 GACAAAACCTCCCTTAACTTGGGAGATTTGCTTGCAGAGCTTGCACCTCTTGGC 900
Db 1055 GACAAAACCTCCCTTAACTTGGGAGATTTGCTTGCAGAGCTTGCACCTCTTGGC 1114
QY 901 ATTTCTTTCTTTGACATTCCTGCGGATTTCTTGGCTCAGGTTTGTGATTAAGATGACA 960
Db 1115 ATTTCTTTCTTTGACATTCCTGCGGATTTCTTGGCTCAGGTTTGTGATTAAGATGACA 1174
QY 961 GAACAAACACCGCAGAAACACTTTGAGAAAGAGAAACCAAGCTGCCAATCTCATTTGAG 1020
Db 1175 GAACAAACACCGCAGAAACACTTTGAGAAAGAGAAACCAAGCTGCCAATCTCATTTGAG 1234
QY 1021 TGTGTTTGGCTGATTTAGGAGTGTAGGAAATCTGTTTCCATTGCAACTGGAAGGCA 1080
Db 1235 TGTGTTTGGCTGATTTAGGAGTGTAGGAAATCTGTTTCCATTGCAACTGGAAGGCA 1294
QY 1081 CACTTGAAGGCTTGGACACCTGACGCTTACCA----- 1115
Db 1295 CACTTGAAGGCTTGGACACCTGACGCTTACCAAGAAAGAAACAGGGAGACATCAAGC 1354
QY 1116 --TCAGAACTTAAGTTTAAAGAGCGAGTGCAGTGCATGAGCCCAAGGGGCGAGATAT 1173
Db 1355 AGTCAGAAAGCTTAAGTTTAAAGAGCGAGTGCAGTGCATGAGCCCAAGGGGCGAGATAT 1414
QY 1174 AAGAGCCGACAGGCTCAGTATGATGACAGAGAGTCCCAAGACCGAATCAACAGCCGAG 1233
Db 1415 AAGAGCCGACAGGCTCAGTATGATGACAGAGAGTCCCAAGACCGAATCAACAGCCGAG 1474
QY 1234 GGCAGTCCCAACCAAGTGAAGAGAGTGAAGCTTCAACGACCGAACCGCTTCCGCGCC 1293
Db 1475 GGCAGTCCCAACCAAGTGAAGAGAGTGAAGCTTCAACGACCGAACCGCTTCCGCGCC 1534
QY 1294 TCGCTGCGCTCAAAAGTTTCTAGCCAAACAGATGATGATGCTGACACAGCCCTTGGC 1353
Db 1535 TCGCTGCGCTCAAAAGTTTCTAGCCAAACAGATGATGATGCTGACACAGCCCTTGGC 1594

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QY 1354 ACTGATGATGTATATGATGAAAAAGATGCGAGTGTATGATCACTGTGAGACCTCAC 1413
Db 1595 ACTGATGATGTATATGATGAAAAAGATGCGAGTGTATGATCACTGTGAGACCTCAC 1654
QY 1414 CCACCACTTTAAAGCTGTATGAGCTATCAGAAATTTATGAATTTTATGTTGCAAAACGG 1473
Db 1655 CCACCACTTTAAAGCTGTATGAGCTATCAGAAATTTATGAATTTTATGTTGCAAAACGG 1714
QY 1474 AAGTTTAAAGAAAGCTTACGTCATATGATGTAAGATGTCTAATGAACTTATGCTTGTGCT 1533
Db 1715 AAGTTTAAAGAAAGCTTACGTCATATGATGTAAGATGTCTAATGAACTTATGCTTGTGCT 1774
QY 1534 GGTGATCTGAGACATGTTGTGTAGAAATTAAGCCCTTCAAAACAGTGTGATCAAAATCTT 1593
Db 1775 GGTGATCTGAGACATGTTGTGTAGAAATTAAGCCCTTCAAAACAGTGTGATCAAAATCTT 1834
QY 1594 GGAAGAGGGCAATATCATATGATTAAGAAAGCCGAGAGAAAAATACACAGAACTGTAG 1653
Db 1835 GGAAGAGGGCAATATCATATGATTAAGAAAGCCGAGAGAAAAATACACAGAACTGTAG 1894
QY 1654 ACCACAGAGATCTAGTATGCTCGGTCGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1713
Db 1895 ACCACAGAGATCTAGTATGCTCGGTCGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1954
QY 1714 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT 1773
Db 1955 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT 2014
QY 1774 GCTGAGCCCTGCTTGGCTTTCATCCAGATCCCACTTTGAAAGTGAACAGACATCT 1833
Db 2015 GCTGAGCCCTGCTTGGCTTTCATCCAGATCCCACTTTGAAAGTGAACAGACATCT 2074
QY 1834 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCGCACAAAACAGTGTGCTC 1893
Db 2075 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTCCGGTTCGCACAAAACAGTGTGCTC 2134
QY 1894 TTATCCAGATCAACTATGTGCAACATCTGAGAGGCTTCAAGTTCATTCGAGCCCAAT 1953
Db 2135 TTATCCAGATCAACTATGTGCAACATCTGAGAGGCTTCAAGTTCATTCGAGCCCAAT 2194
QY 1954 GAGTTAGAGCCGAGCTTTCTAGAGGCTTAAAGCCCTAATATGACAGTCAAGCAACAG 2013
Db 2195 GAGTTAGAGCCGAGCTTTCTAGAGGCTTAAAGCCCTAATATGACAGTCAAGCAACAG 2254
QY 2014 GTGCCAATTAGTCAAAAGCGATGCTCAGAGTGGCAGCCACCAACCACTTGCACAA 2073
Db 2255 GTGCCAATTAGTCAAAAGCGATGCTCAGAGTGGCAGCCACCAACCACTTGCACAA 2314
QY 2074 ATTAATAGGCGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCA 2133
Db 2315 ATTAATAGGCGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCA 2374
QY 2134 GGCATCAAGCATCTGCCAGGCGAGAAAGCTGCAACCTTAACCTGACAGGCTTACAGGAA 2193
Db 2375 GGCATCAAGCATCTGCCAGGCGAGAAAGCTGCAACCTTAACCTGACAGGCTTACAGGAA 2434
QY 2194 AGCATTTTGAAGTCAACACTGCTTGTGCTTCCAGAGAAATGTTGAGTTGACAG 2253
Db 2435 AGCATTTTGAAGTCAACACTGCTTGTGCTTCCAGAGAAATGTTGAGTTGACAG 2494
QY 2254 TCMAATCTCAACAGAGACGTTTCTATGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2313
Db 2495 TCMAATCTCAACAGAGACGTTTCTATGAGAAAAAGCTTTGACATGGAGAGAACTCTG 2554
QY 2314 TTGTCTGTCTGCTCCATGCTGCGAGAGAACTTGGGGGAAATCTTTGCTGAGCAAACTG 2373
Db 2555 TTGTCTGTCTGCTCCATGCTGCGAGAGAACTTGGGGGAAATCTTTGCTGAGCAAACTG 2614
QY 2374 ATCAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGGCTCAGA 2433
Db 2615 ATCAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGGCTCAGA 2674
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QY 2434 GGCAGCCAGATTTTACCCTCAATGAGGGAAATCCAAATGTTTATTAACCTGATAGAG 2493
Db 2675 GGCAGCCAGATTTTACCCTCAATGAGGGAAATCCAAATGTTTATTAACCTGATAGAG 2734
QY 2494 GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCGGACCGCAGCTGCCAGGGAA 2553
Db 2735 GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCGGACCGCAGCTGCCAGGGAA 2794
QY 2554 GCTGCTTTGATCAGACTCTCTTAAGACTGGAAGTCAAGATCACTCAGAGCAATTTGT 2613
Db 2795 GCTGCTTTGATCAGACTCTCTTAAGACTGGAAGTCAAGATCACTCAGAGCAATTTGT 2854
QY 2614 AAGCAGAGAAAGTACAGATGCGCTTCAAGCTTGCTTCTCATGTCAAACTGAATTA 2667
Db 2855 AAGCAGAGAAAGTACAGATGCGCTTCAAGCTTGCTTCTCATGTCAAACTGAATTA 2908

RESULT 14
US-10-313-542-303
; Sequence 303, Application US/10313542
; Publication No. US20030120057A1
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/10/313,542
; CURRENT FILING DATE: 2002-12-05
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US/09/495,050
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030120057A1 4970006CT1
US-10-313-542-303

Query Match 19.1%; Score 509.8; DB 15; Length 582;
Best Local Similarity 99.4%; Pred. No. 2.3e-146;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1594 GGAAGAGGGCAATATCATATGATTAAGAAAGCCGAGAGAAAAATACACAGAACTGTAG 1653
Db 1 GGAAGAGGGCAATATCATATGATTAAGAAAGCCGAGAGAAAAATACACAGAACTGTAG 60
QY 1654 ACCACAGAGATCTAGTATGCTCGGTCGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1713
Db 61 ACCACAGAGATCTAGTATGCTCGGTCGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 120
QY 1714 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT 1773
Db 121 ATAGAGTCCAGCTGAGCTGCTTACTAGACATCTATCAACAGTCTCTTGGAAAGGCTCT 180
QY 1774 GCTGAGCCCTGCTTGGCTTTCATCCAGATCCCACTTTGAAAGTGAACAGACATCT 1833
Db 181 GCTGAGCCCTGCTTGGCTTTCATCCAGATCCCACTTTGAAAGTGAACAGACATCT 240
QY 1834 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGGTTCGCACAAAACAGTGGCTGC 1893
Db 241 GACTATCAAGCCCTGTGATAGCAAAAGATCTTTGGGGTTCGCACAAAACAGTGGCTGC 300
QY 1894 TTATCCAGATCAACTATGTGCAACATCTGAGAGGCTTCAAGTTCATTCGAGCCCAAT 1953
Db 301 TTATCCAGATCAACTATGTGCAACATCTGAGAGGCTTCAAGTTCATTCGAGCCCAAT 360
QY 1954 GAGTTAGAGCCGAGCTTTCTAGAGGCTTAAAGCCCTAATATGACAGTCAAGCAACAG 2013
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Db 361 GAGTTCAAGTGGCCAGACCTTTCTAGCGCTTAGCCCTTACTATGCAAGTCAAAGCAGACAG 420
 Oy 2014 GTGCCAATTAGTCAAAGCGATGCTCTAGCAAGTGGCAGCCACCAACACCATTTGCCAACCA 2073
 Db 421 GTGCCAATTAGTCAAAGCGATGCTCTAGCAAGTGGCAGCCACCAACCATTTGCCAACCA 480
 Oy 2074 ATAAATACGGCAGCCAGCCAGCCAGCCCAACAACCTTACAGATC 2118
 Db 481 ATAAATACGGCAGCCAGCCAGCCAG -CCCAACAACCTTACAGATC 524

RESULT 15
US-10-353-690-55
; Sequence 55, Application US/10353690

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APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
APPLICANT: Galvin, Katherine M.
APPLICANT: Healy, Aileen
APPLICANT: Acton, Susan L.
APPLICANT: Donoghue, Mary
APPLICANT: Stagliano, Nancy
APPLICANT: Perodin, Jacqueline
APPLICANT: Rodriguez-Way, Amelie
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395
TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 11720
TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3464, 345, 9252, 9135,
TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
TITLE OF INVENTION: 283, 2254, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
FILE REFERENCE: MP102-018P1MONNIM
CURRENT APPLICATION NUMBER: US/10/353,690
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: 60/353,224
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/354,529
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/373,861
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: 60/388,080
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: 60/390,971
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/394,130
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/394,797
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: 60/404,904
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/405,450
PRIOR FILING DATE: 2002-08-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 2335
TYPE: DNA
ORGANISM: Homo Sapiens
IS-10-353-690-55

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Query Match	18.4%	Score 492;	DB 17;	Length 2335;
Best Local Similarity	59.3%	Pred. No. 2e-140;		
Matches 1087; Conservative	0;	Mismatches 555;	Indels 192;	Gaps 7

QY 217 TACCGGCGGTGCAGAACTACCTGTATCAACGTCGTGAGAGACCCCGCGGCTGGCGTTT 276

D	320	TACGCGCGCCTGCAAGAACTGGGATCTACAACGTGCTGAGCGGCGCGGCGCTGGGCGCTTC	379
O	277	ATCTACCAACGCTTTGCTTTTCTCTCTTGCTTTGGTGGCTTGATTTTGTCAAGTGTTTCT	336
D	380	GCTACCAACGCTTTCATATTTTGTGTGCTTTCAAGCTCGTGGTGTCTGTGTGTCTGTC	439
O	337	ACCATCTTGAGCACACAAAATTGGCGCTCAAGTTGCCCTTGATGTCCTGAGAGTTGCTGATG	396
D	440	ACTATCCAGGAGCAACAGAACTTGGCCACAAGAGTCTCTCATCTTTGAAATTCGTGATG	499
O	397	ATTGTCGCTTTGGTTTGGAGTTCAATCATTTGGAATCTGCTGCGGGGTGTGCTGTGTGA	456
D	500	ATCTGGTCTTTCGGCTTGGATCAATGCTCCGGGTCTGTGTCCGCGAGTCTGCTGCGCG	559
O	457	TATAGAGATGGCAAGAAAGACTGAGGTTTGTCTGAAAAGCCCTTCTGTATATGATAC	516
D	560	TACGAGGATGGCAGGGTCCGCTTCGGTTTGCAGAAAAGCCCTTCTGTATGATGACTTC	619
O	517	ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGAAAATCTCAGGGTAAATATTTTGGC	576
D	620	ATCTGTTTCGGGCTCGGTGGCGTCAATCCCGGGGTACCAAGGGCAATCTTCCGC	679
O	577	ACGCTCGACTCAGAAAGCTCCGTTTCCCTACAGATCCCGCATGATGATGGACGGA	636
D	680	ACGTCGCGCTCGCGAGCATCGCTCTCTGCAAGATCTGCGCATGATGATGGACGCG	739
O	637	AGGGGAGGCACTTGGAATAATCTGGGTTTCACTGATGTTATGCTCAACAGCAAGAAATTAATC	696
D	740	CGGGCGGCACTTGGAAGTGTCTGGGCTCAATGGTCTAGCGCATAGCAAGAGCTGATC	799
O	697	ACAGCTTGATCATAGGATTTTGGTCTTAATTTTTCGCTTTCCTTGTCTATCTGTG	756
D	800	ACCCCTGATGATCACTGGGTTCTGTGTCTCAATCTTCGCTCTTCTGATCTGACCTGACC	859
O	757	GAAAAGATGCAATPAAAGTTTCTCAATATACAGATGCTCTGCTGGTGGGGCAATTT	816
D	860	GAGAAAGACGCAACTCCGACTTCTCTCTACGCGACTGCTCTGTGTGGGAGCATTT	919
O	817	ACATTGCAACATATTGCTATGATGAGACAAAATCCCTCAATCTGATGGAGATTTGCTT	876
D	920	ACATTTGCAACATCTGGGTATGATGAGACACCGCACATATGGTGGGCAAGGTCCTG	979
O	877	CTGCAAGGCTTTGCATCTCTTGGCATTTCTTTCTTTGCACTTCTCGCCGGCATTTCTGGC	936
D	980	GCTCTGAGCTTCGCTTACTGAGGCAATCTTTCTTTGCTGCTGCGCGCATCTTAAGC	1039
O	937	TCAGTTTGTGATTAAGTACAGAACACACCGCCAGAAACATTTGACAAAGAAAG	996
D	1040	TTCGGCTTTTGGCTCGAAGGTCTCAGAGACAGACCGGACAAAGCACTTGCAGAACCGAGG	1099
O	997	AACCACTGCGCAACTCATTCAGTGTGTGTGGCGTATTTACGAGCTGATGAGAAATCT	1056
D	1100	ATGCGCGGACGCAACTCATTCAGGCTGTCCGGCGCTGTACTCACCAGATATGAGCCGG	1159
O	1057	GTTTTCATTGCAACTGGAAGCCCACTTGAAGGCTTTCACAC-----	1100
D	1160	GCTACTGACAGCACCTGGTACTACTATGACAGTATCTTCATCCATCTTCAGAGAGCTG	1219
O	1101	-----	1100
D	1220	GCCCTTGTTTGAGACGTGACCGGACCGCAATGGGGGCTTACGCGCCCTGAGAGTG	1279
O	1101	-----	1100
D	1280	CGGCGGGCGCGGTATCCGACGAGACACCTCCCGTTATCCGCGCGCTTGCACCTGCGAC	1339
O	1101	-----CTGACGCCCTTACCAATCAGAAAGCTAATTTTAAAGACGA	1140
D	1340	CGGCGGGAGACACTCTCTCTGCGCTGGGAAAGACGCGGATGGGCATCAAGACGCG	1399
O	1141	GTGGGATGTGCTAGCCCGCAGGGGCAAGATTT-----AAGAGCGCAAGCTCTGAT	1194
D	1400	ATTCGATATGGCAGCTCTCCAGCGCGGACGGGTCTTCCAAAGCAGCAGCTGGACCTTCA	1459

1280 CGGCGGGGCGCGGTAACCGGACGGAGGACCTCCCGTTACCGCGCGGTTCCACCTCGCAC 1339
1101 -----CTGAGCGCTACCAATCAGAAAGTAAAGTAAAGGAGA 1140
1340 CGGCGGGGACGACCTCTCTTCTGCGCTCGGGGAAAGACCGCGATGGGCAATCAAGACCCG 1399
1141 GTGCGCATGCTAGCGCCCGAGGGGCGAAGATATT-----AAGCGCGACAAAGCCTCACTA 1194
1400 ATTCGATATGGGAGCTCTCCACCGCGGACGGAGCTTCCAAACGACGAGCTGGCACCTTCA 1459

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QY 1195 GGTGACAGGAGGTCCCCAAGACCGACATCACAGCCGAG---GCAGTCCACCAAAAGTG 1251
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Db 1460 ACAATGCCACCTCCCCAAGACCGACAGGTGGTGAAGGCCACAGCCCAACCAAGTG 1519
      |||||
QY 1252 CAGAAAGCTGAGAGCTTCAACGACCGACCCGCTTCCGGCCCTCGCTCGCTCAAAAGT 1311
      |||||
Db 1520 CAAMAAGCTGAGAGCTTCAATGACCCGACCCGCTTCCGGGCATCTTGAGACTC----- 1573
      |||||
QY 1312 TCTCAGCCAAACACAGTATGATGTGACACAGCCCTTGSCATGATGATATATGAT 1371
      |||||
Db 1574 -----AAACCCCGCACCTTGTCTGAGAGATGCC---CTCAGAGAAATGACAGAG 1621
      |||||
QY 1372 GAAAAAGATGCCAGTGTATGTATCATGTGAGAGACCTGACCCACACTTAAACTGTC 1431
      |||||
Db 1622 GAGAAAGAGCTACCAAGTGTGAGCTCACGATGAGACGATCATGCTGCTGAAAGACAGTC 1681
      |||||
QY 1432 ATTGAGCTATCGAATTATGAAATTTCAATGTTGCAAAAACGAAAGTTTAAAGAAAGTTA 1491
      |||||
Db 1682 ATCCGCTCATGAGATTCATCAAGTTCCTGTGGCCAAAAGAAATTCAAAGAGACACTG 1741
      |||||
QY 1492 CGTCCATATGATGTAAAGATGTCAATTGAAACATATTTCTGTGTCATCTGGACATGTTG 1551
      |||||
Db 1742 CGACCTAGACCTGAAAGAGCTGATTTGACAGTACTCAGCAGGCCACCTGGACATGCTG 1801
      |||||
QY 1552 TGTAGAATTAAAAACCTTCAAACACGATGTGATCAAAATTTCTGAAAAAGGC---AAATC 1608
      |||||
Db 1802 GGCCTGATCAAGAGCTGCAAACTCGGATGAGACCAAAATTTGTGGTGGGGGCCCGGGGAGC 1861
      |||||
QY 1609 ACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGAAATGAGACCAAGACGATCTC 1668
      |||||
Db 1862 AGAAAGGCCCGGAGAAAGGCCGACAAAGGGCCCTCCGACCGAGAGGTGGTGAATGAATC 1921
      |||||
QY 1669 AGTATGCTCGTGGGTGGTCAAGGTTGAATAAAACAGTACAGTCAATAGAGTCCAAAGCTG 1728
      |||||
Db 1922 AGCATATGGGACGCTGGTCAAGGTGAGAAAGAGTGAATGCAATCGAGCACAAGCTG 1981
      |||||
QY 1729 GACTGCTACTAGACATCTATCAACAGGTCCTTGGAAAAGGCTCTGCAAGCCTCGCT 1788
      |||||
Db 1982 GACTGCTGTGGGCTTCTATTCGCGCTGCTGC-----GCTCTGGCACTCGGCCAGC 2035
      |||||
QY 1789 TTGGCTTCATTCAGATCCCACTTTGAAATGGAACAGACATCTGACTATCAAAAGCCT 1848
      |||||
Db 2036 CTGGGCGCGTGCAAGTGCCTGCTTCGACCCGACATCACCTCGACTACCAAGCCCT 2095
      |||||
QY 1849 GTGATAGCAAGAATCTTTCGGGTTCCGCACAA 1882
      |||||
Db 2096 GTGGACCAAGAGACATCTCTCGTCCGACAGA 2129
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Search completed: October 23, 2005, 19:13:17
Job time : 1378.34 secs